OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: February 6, 2005, 05:55:14 ; Search time 6352 Seconds
                (without alignments)
                11331.065 Million cell updates/sec

Title: US-09-967-237A-1
Perfect score: 1522
Sequence: 1 acagtcagccgccatggctcc..........ttaaaataaatattatat 1522
Scoring table: OLIGO_NUC
                Gapop_60.0 , Gapext 60.0
Searched: 4526729 seqs, 2364849745 residues
Word size :   50
Total number of hits satisfying chosen parameters: 146
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1522	100.0	1522	6	AR074439	AR074439 Sequence
2	1522	100.0	1522	6	AR081119	AR081119 Sequence
3	1522	100.0	1522	6	AR085316	AR085316 Sequence
4	1522	100.0	1522	6	AR088064	AR088064 Sequence
5	1522	100.0	1522	6	AR104223	AR104223 Sequence
6	1522	100.0	1522	6	AR143487	AR143487 Sequence
7	1522	100.0	1522	6	AR171392	AR171392 Sequence
8	1522	100.0	1522	6	AR171563	AR171563 Sequence
9	1522	100.0	1522	6	BD243152	BD243152 MN gene a
10	1522	100.0	1522	6	CQ834035	CQ834035 Sequence
11	1522	100.0	1522	6	AX330007	AX330007 Sequence
12	1522	100.0	1522	6	AX332607	AX332607 Sequence
13	1522	100.0	1522	6	AX333244	AX333244 Sequence
14	1522	100.0	1522	6	AX336174	AX336174 Sequence
15	1522	100.0	1552	9	HSMATUMN	X66839 H.sapiens M
16	1522	100.0	1639	9	BC014950	BC014950 Homo sapi
17	1491	98.0	1519	9	HAJ10588	AJ010588 Homo sapi
18	1399	91.9	1399	6	AR095263	AR095263 Sequence
19	888	58.3	1289	6	CQ726696	CQ726696 Sequence
20	365	24.0	6521	6	CQ806582	CQ806582 Sequence
21	365	24.0	6521	6	AX795690	AX795690 Sequence
22	365	24.0	6521	6	AX822141	AX822141 Sequence
23	365	24.0	6521	6	AX825781	AX825781 Sequence
24	365	24.0	10898	6	AR074442	AR074442 Sequence
25	365	24.0	10898	6	AR081122	AR081122 Sequence
26	365	24.0	10898	6	AR083319	AR083319 Sequence
27	365	24.0	10898	6	AR085319	AR085319 Sequence
28	365	24.0	10898	6	AR080067	AR080067 Sequence
29	365	24.0	10898	6	AR104226	AR104226 Sequence
30	365	24.0	10898	6	AR143490	AR143490 Sequence
31	365	24.0	10898	6	AR171566	AR171566 Sequence
32	365	23.9	10898	6	BD241155	BD241155 MN gene a
33	365	24.0	88328	6	AL357874	AL357874 Human DNA
34	365	24.0	187856	9	AF334829	AF334829 Homo sapi
35	364	23.9	415	6	AR074454	AR074454 Sequence
36	364	23.9	415	6	AR081134	AR081134 Sequence
37	364	23.9	415	6	AR085331	AR085331 Sequence
38	364	23.9	415	6	AR080079	AR080079 Sequence
39	364	23.9	415	6	AR104238	AR104238 Sequence
40	364	23.9	415	6	AR143502	AR143502 Sequence
41	364	23.9	445	6	AR171406	AR171406 Sequence
42	364	23.9	445	6	AR171577	AR171577 Sequence
43	364	23.9	445	6	BD243167	BD243167 MN gene a
44	331	21.7	331	6	CQ667014	CQ667014 Sequence
45	314	20.6	592	6	CQ724691	CQ724691 Sequence

ALIGNMENTS

RESULT 1
AR074439
AR074439

LOCUS   AR074439   1522 bp   DNA   linear   PAT 28-AUG-2000
DEFINITION Sequence 1 from patent US 5955075.
ACCESSION   AR074439
VERSION   AR074439.1 GI:10001194
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 1 21-SEP-1999;
FEATURES   Location/Qualifiers
     source   1..1522
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACAGTCAGCCGCCATGGCTCCCCGGGTTGCCCCAGGCCGGCTCCCTCGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACAGTCAGCCGCCATGGCTCCCCGGGTTGCCCCAGGCCGGCTCCCTCGTTGATCCCGGCC 60

Qy   61 CCTGCTCCCAGGCCCTCACTGTGCCAACTGCTCGCTTCTGATGCCTGGCCCAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTGCTCCCAGGCCCTCACTGTGCCAACTGCTCGCTTCTGATGCCTGGCCCAT 120

Qy 121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTTCTGGGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTTCTGGGGAA 180

Qy 181 GATGACCCACTGGGCGGAGGAGGATTCACCCGAGTGAAGAGAGGAGGATTCACCCGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GATGACCCACTGGGCGGAGGAGGATTCACCCGAGTGAAGAGAGGAGGATTCACCCGAGGAT 240

Qy 241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGATCTACCT 300

First alignment (continued), Query (Qy) vs Database (Db):

```
Qy   241 CCACCCGGAGGAGGAGGAGATCTACCTGGAGGAGGATCTACCT 300
         |||||||||||||||||||||||||||||||||||||||||||
Db   301 GAAGTTAAGCCTAAATCAGAAGAGAAGAAGGATCTACCTACTGTT 360

Qy   301 GAAGTTAAGCCTAAATCAGAAGAGAAGAAGGATCTACCTACTGTT 360
         |||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCTCGGAGGATCCTCAAGAACCCCAGAATAATGCCCAC 420

Qy   361 GAGGCTCTCGGAGGATCCTCAAGAACCCCAGAATAATGCCCAC 420
         |||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGAGTCATTGGGCGCTATGGAGGGGAGGGACCCTGGCCTGC 480

Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGGGAGGGACCCTGGCCTGC 480
         |||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCGGGCCGCTTCAGTCCCGGTGGATATCCCGGCGCTTCGCGCTTC 540
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RESULT 2
LOCUS       AR081119                1522 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5972353.
ACCESSION   AR081119
VERSION     AR081119.1  GI:10007847
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN protein, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1..1522
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match     100.0%;  Score 1522;  DB 6;  Length 1522;
  Best Local Similarity   100.0%;
  Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Second alignment, Query (Qy) vs Database (Db):

```
Qy     1 ACAGTCAGCCGCAATGGCTCCCCTGTCCCCAGCCCCTCCCTCTTGGAT 60
         |||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ACAGTCAGCCGCATGGCTCCCCTGTCCCCAGCCCCTCCCTCTGTTGGAT 60
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DEFINITION  Sequence 1 from patent US 5981711.
ACCESSION   AR085316
VERSION     AR085316.1  GI:10012085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J.; Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 1 09-NOV-1999;
FEATURES             Location/Qualifiers
  source          1..1522
                  /organism="unknown"
                  /mol_type="unassigned DNA"
ORIGIN
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Query Match          100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity 100.0%;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Right-hand alignment column (Qy = query, Db = database), positions 1–780:

```
Qy    1 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGCCCCCCTGGCTCTCCCTCTGTTGATCCCGGCC   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGCCCCCCTGGCTCTCCCTCTGTTGATCCCGGCC   60

Qy   61 CCTGCTCCAGGCCCTCACTCTGCAACTGCTGCTCGTGTTCTTGATGCCCAT             120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTGCTCCAGGCCCTCACTCTGCAACTGCTGCTCGTGTTCTTGATGCCCAT             120

Qy  121 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGAGGAATTCCCCGTTGGGAGGAGGCTCTTCTGGGGAA  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGAGGAATTCCCCGTTGGGAGGAGGCTCTTCTGGGGAA  180

Qy  181 GATGACCCACTGGGCGGAGGAGGATCTGCCCCAGTGAAGAGGAGGATCTACCT             240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GATGACCCACTGGGCGGAGGAGGATCTGCCCCAGTGAAGAGGAGGATCTACCT             240

Qy  241 CCACCCGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT                   300
        ||||||||||||||||||||||||||||||||||||||||||||
Db  241 CCACCCGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT                   300

Qy  301 GAAGTTAAGCCTAAATCAGGAAGAAGAGGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT    360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GAAGTTAAGCCTAAATCAGGAAGAAGAGGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT    360

Qy  361 GAGGCTCCTGGAGATCCTCAAAGAACCCCAGAAATAATCGCCCAGAGAAGGGGAT          420
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GAGGCTCCTGGAGATCCTCAAAGAACCCCAGAAATAATCGCCCAGAGAAGGGGAT          420

Qy  421 GACCAGAGAGTCATTGGCGCTATGGAGGGCGACCCGCGCCCGGGTGTCCCAGCCTGC        480
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GACCAGAGAGTCATTGGCGCTATGGAGGGCGACCCGCGCCCGGGTGTCCCAGCCTGC        480

Qy  481 GCGGGCCGCTTCCAGTCCCCGGTGGAATATCGCCGCGCCCTTCGCGCCGCC             540
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GCGGGCCGCTTCCAGTCCCCGGTGGAATATCGCCGCGCCCTTCGCGCCGCC             540

Qy  541 CTGCGCCCCCTGGAACTCTCTGGGCTTCCCGCGCCGCCTCCCAGAACTGCGCCGCTGCGC     600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CTGCGCCCCCTGGAACTCTCTGGGCTTCCCGCGCCGCCTCCCAGAACTGCGCCGCTGCGC     600

Qy  601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCCTGGGCTCGAGATGGCTCTGGGTCCC    660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCCTGGGCTCGAGATGGCTCTGGGTCCC    660

Qy  661 GGGCCGGGGACTACCGGGCTCTGCAGCTGCAGGTCGTCCGGGGC                    720
        |||||||||||||||||||||||||||||||||||||||||||
Db  661 GGGCCGGGGACTACCGGGCTCTGCAGCTGCAGGTCGTCCGGGGC                    720

Qy  721 TCGGAGCGCACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGTTCACCTCAGC   780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TCGGAGCGCACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGTTCACCTCAGC   780
```

Left-hand alignment column (Qy = query, Db = database), positions 541–1522:

```
Qy  541 CTGCGCCCCCTGGAACTCTCTGGGCTTCCCGCGCCGCCTCCCAGAACTGCGCCGCTGCGC     600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CTGCGCCCCCTGGAACTCTCTGGGCTTCCCGCGCCGCCTCCCAGAACTGCGCCGCTGCGC     600

Qy  601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCCTGGGCTCGAGATGGCTCTGGGTCCC    660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCCTGGGCTCGAGATGGCTCTGGGTCCC    660

Qy  661 GGGCCGGGGACTACCGGGCTCTGCAGCTGCAGGTCGTCCGGGGC                    720
        |||||||||||||||||||||||||||||||||||||||||||
Db  661 GGGCCGGGGACTACCGGGCTCTGCAGCTGCAGGTCGTCCGGGGC                    720

Qy  721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGTTCACCTCAGC      780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGTTCACCTCAGC      780

Qy  781 ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGCGGCCTGGCCTGTTGGCC             840
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGCGGCCTGGCCTGTTGGCC             840

Qy  841 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGCCTAATGAGCAGTTGCTCTGCGCTTG  900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGCCTAATGAGCAGTTGCTCTGCGCTTG  900

Qy  901 GAAGAAATCGCTGGAGGAAGGCTCAGGTCCCAGGACTGGACTACAGCTGACTCTCGGTTGACATTATCTGCACTC  960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GAAGAAATCGCTGGAGGAAGGCTCAGGTCCCAGGACTGGACTACAGCTGACTCTCGGTTGACATTATCTGCACTC  960

Qy  961 CTGCCCTCTGACTTCAGCGCGTACTTCCAAATATGAGGGGTCTTCTGACTACACACGCCCTGT    1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 CTGCCCTCTGACTTCAGCGCGTACTTCCAAATATGAGGGGTCTTCTGACTACACACGCCCTGT    1020

Qy 1021 GCCCAGGGGTGTGCTGCCCAGGGAAGAAAAACAGTGCCTATGAGCAGTTGCGTTGCCTGCTC    1080
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Db 1021 GCCCAGGGGTGTGCTGCCCAGGGAAGAAAAACAGTGCCTATGAGCAGTTGCGTTGCCTGCTC    1080

Qy 1081 CACACCCCTCTCTGACACCCTGTGGGGACTCTGGTGACTCTGGGTTCACCAGCCTACTT      1140
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Db 1081 CACACCCCTCTCTGACACCCTGTGGGGACTCTGGTGACTCTGGGTTCACCAGCCTACTT      1140

Qy 1141 GCGGACGGCAGCCTTTGAATGGGCCGAGTGATTGAGGCCTTCCTTCCCTGCTCCTCCGGACAGC  1200
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GCGGACGGCAGCCTTTGAATGGGCCGAGTGATTGAGGCCTTCCTTCCCTGCTCCTCCGGACAGC  1200

Qy 1201 AGTCCTCGGGCTCGGAGCCAGTGAAGTTCCTGCCTCTGGTCTGCTGCTGGTGACTCCTA     1260
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Db 1201 AGTCCTCGGGCTCGGAGCCAGTGAAGTTCCTGCCTCTGGTCTGCTGCTGGTGACTCCTA     1260

Qy 1261 GCCCTGGTTTTTGGCTTCCTTTTTTGGCTGTGTCACAGGCGTTCCTTGTGCAGATGAGA     1320
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Db 1261 GCCCTGGTTTTTGGCTTCCTTTTTTGGCTGTGTCACAGGCGTTCCTTGTGCAGATGAGA     1320

Qy 1321 AGGCAGCACAGAAGGGAACCAAAGGGGGTGTGAGCTACACGGTGAGGTTAGCCGAG        1380
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGGCAGCACAGAAGGGAACCAAAGGGGGTGTGAGCTACACGGTGAGGTTAGCCGAG        1380

Qy 1381 ACTGGGAGCCTAGAGGCTGGATCTTGGAGAATGTGGAGGCATCAGCCATCTGAGGG        1440
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Db 1381 ACTGGGAGCCTAGAGGCTGGATCTTGGAGAATGTGGAGGCATCAGCCATCTGAGGG        1440

Qy 1441 GGAGCCCGGTAACTGTCTCTGCTCATTATGCCCACTTCCTTTTAACTGCCAAGAAATT      1500
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Db 1441 GGAGCCCGGTAACTGTCTCTGCTCATTATGCCCACTTCCTTTTAACTGCCAAGAAATT      1500

Qy 1501 TTTTAAAATAAATATATTTATAAT   1522
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Db 1501 TTTTAAAATAAATATATTTATAAT   1522
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RESULT 3
AR085316
LOCUS       AR085316               1522 bp    DNA     linear   PAT 01-SEP-2000
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Qy   781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840

Qy   841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900

Qy   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy   961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020

Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080

Qy   1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140

Qy   1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200

Qy   1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1260
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Db   1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1320

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
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Db   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380

Qy   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
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Db   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440

Qy   1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Db   1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAATATTTATAAT 1522
              ||||||||||||||||||||||
Db   1501 TTTTAAAATAAATATTTATAAT 1522

RESULT 4
AR088064
LOCUS   AR088064   1522 bp   DNA   linear   PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5989838.
ACCESSION   AR088064
VERSION   AR088064.1 GI:10014827
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 1 23-NOV-1999;
FEATURES   Location/Qualifiers
     source   1. .1522
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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  Query Match             100.0%;  Score 1522;  DB 6;  Length 1522;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 60

Qy         61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 120

Qy        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Qy        181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240

Qy        241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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Db        241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Qy        301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
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Db        301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Qy        361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
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Qy        421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
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Qy        481 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 540
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Qy        541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGC 600
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Db        541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGC 600

Qy        601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
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Db        601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660

Qy        661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC 720
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Db        661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC 720

Qy        721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780

Qy        781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840
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Db        781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840

Qy        841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900

Qy        901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
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Db        901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy        961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
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Db        961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020

Qy       1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
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RESULT 5
LOCUS   AR104223   1522 bp   DNA   linear   PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6093548.
ACCESSION   AR104223
VERSION   AR104223.1 GI:12816931
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 1 25-JUL-2000;
FEATURES   Location/Qualifiers
     source   1..1522
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match   100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy   1 ACAGTCAGCCGCGCAATGGCTCCCGTGTCCCCGTGTGCCCCGCGCTCCCTCGTCTCGTTGATCCCGGCC 60

Db   1 ACAGTCAGCCGCGCAATGGCTCCCGTGTCCCCGTGTGCCCCGCGCTCCCTCGTCTCGTTGATCCCGGCC 1080

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Qy  1261 GCCCTGGGTTTTTGGGCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTCGTGTCAGATGAGA 1320
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Db  1261 GCCCTGGGTTTTTGGGCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTCGTGTCAGATGAGA 1320

Qy  1321 AGGCAGCACAGAGAGGCGGAACCAAAGGGGGTGTGAGCGTACCGGCCCCAGCAGAGGTAGCCGAG 1380
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Db  1321 AGGCAGCACAGAGAGGCGGAACCAAAGGGGGTGTGAGCGTACCGGCCCCAGCAGAGGTAGCCGAG 1380

Qy  1381 ACTGGAGCCCTAGAGGCTGGATCTTGGAGAAATGAGAAGCCAGAGGCCATCTGAGGG 1440
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Qy  1441 GGAGCCGGGTGAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Db  1441 GGAGCCGGGTGAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500

Qy  1501 TTTTAAAATAAAATATTTTATAAT 1522
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Db  1501 TTTTAAAATAAAATATTTTATAAT 1522
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RESULT 6

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LOCUS       AR143487               1522 bp    DNA      linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6204370.
ACCESSION   AR143487
VERSION     AR143487.1  GI:15104773
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 1 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1..1522
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ORIGIN
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     1 ACAGTCAGCCGCCATGGCTCCCTGTCCCCTGCCCCTGGCCTCCCTCCTTCGTTGATCCCGCC 60

Qy    61 CCTGCTCCAGGCCCTCACTGCTGCTCGCTCGCTCCTTGCTGCTGTGCCTGCTTCGATGCTCCAT 120
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Db    61 CCTGCTCCAGGCCCTCACTGCTGCTCGCTCGCTCCTTGCTGCTGTGCCTGCTTCGATGCTCCAT 120

Qy   121 CCCCAGAGGGTTGCCCCGGATGCAGGAGGAATTCCCCCCTTGGGCGAGGACTCTTTCTGGGGAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCCAGAGGGTTGCCCCGGATGCAGGAGGAATTCCCCCCTTGGGCGAGGACTCTTTCTGGGGAA 180

Qy   181 GATGACCCACTGGGCGGAGGATCTGCCCGGAGGATTCACCCAGTGAAGGATCACCCAGGGAT 240
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Db   181 GATGACCCACTGGGCGGAGGATCTGCCCGGAGGATTCACCCAGTGAAGGATCACCCAGGGAT 240

Qy   241 CCACCCCGGAGGAGGAGGATCTACCTGGACGAGGACGGAGGATCTACCT 300
         ||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACCCCGGAGGAGGAGGATCTACCTGGACGAGGACGGAGGATCTACCT 300

Qy   301 GAAGTTAAGCCTAAAATCAGAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAAGTTAAGCCTAAAATCAGAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Qy   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAGAATAATGCCACAGGGACAAAGAAGGGGAT 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAGAATAATGCCACAGGGACAAAGAAGGGGAT 420

Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGCAACCCCGGGTGTCCCCAGCCTGC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGAGTCATTGGGCGCTATGGAGGCAACCCCGGGTGTCCCCAGCCTGC 480
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Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGCAACCCCGGGTGTCCCCAGCCTGC 480
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Db   421 GACCAGAGTCATTGGGCGCTATGGAGGCAACCCCGGGTGTCCCCAGCCTGC 480

Qy   481 GCGGGGCACGGCGTTCCAGTCCCGGGGTGGATAATCGCGGGCCCGCCCAGCTTGGCGCCCGGGCC 540
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Db   481 GCGGGGCACGGCGTTCCAGTCCCGGGGTGGATAATCGCGGGCCCGCCCAGCTTGGCGCCCGGGCC 540

Qy   541 CTGCGCCCCCCTGGAACTCCTGGGCTTCAGCGTCCCGCTCCCAGAACTGCCGGCGCGC 600
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Db   541 CTGCGCCCCCCTGGAACTCCTGGGCTTCAGCGTCCCGCTCCCAGAACTGCCGGCGCGC 600

Qy   601 AACAATGGGCACCACAGTGTGCAAACTGACCCTGCCCTCCCTGGGTCCCTAGAGATGGCTCTGGGTCCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACAATGGGCACCACAGTGTGCAAACTGACCCTGCCCTCCCTGGGTCCCTAGAGATGGCTCTGGGTCCC 660

Qy   661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCTGCGGGC 720
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Db   661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCTGCGGGC 720

Qy   721 TCGGAGCACACTGTGGAAGGCACCACCGTTTCCCTGCCCGAGATCCACACGCTGTTCACCTCAGC 780
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Db   721 TCGGAGCACACTGTGGAAGGCACCACCGTTTCCCTGCCCGAGATCCACACGCTGTTCACCTCAGC 780

Qy   781 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTCGGGCGCCCGGGGAGGCCCTGGCGTTGGCC 840
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Db   781 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTCGGGCGCCCGGGGAGGCCCTGGCGTTGGCC 840

Qy   841 GCCTTTCTGGGAGGAGGGGCCCCGGAAGGAAAACAGTGCCTATGGAGCAGTTGCTGCTGCGTG 900
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Db   841 GCCTTTCTGGGAGGAGGGGCCCCGGAAGGAAAACAGTGCCTATGGAGCAGTTGCTGCTGCGTG 900

Qy   901 GAAGGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCCAGGAGACTGGACATATCTGCACTC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAAGGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCCAGGAGACTGGACATATCTGCACTC 960

Qy   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGTCTCTGACTCACACCCCCGT 1020
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Db   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGTCTCTGACTCACACCCCCGT 1020

Qy  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACACAGTGAATGCTGAGTGCTAAGCAGCTC 1080
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Db  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACACAGTGAATGCTGAGTGCTAAGCAGCTC 1080

Qy  1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTCGGCGTACAGCTGAACTTCCGA 1140
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Db  1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTCGGCGTACAGCTGAACTTCCGA 1140

Qy  1141 GCGACGCAGCCTTTGAATGGGCGGAGTGAGTTGAGGGCGCTCCTTCCCCTGCTGGTGGTGGACAGC 1200
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Db  1141 GCGACGCAGCCTTTGAATGGGCGGAGTGAGTTGAGGGCGCTCCTTCCCCTGCTGGTGGTGGACAGC 1200

Qy  1201 AGTCCTCGGGCGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCCTGCGTCTGGTGGTGGTGGACATCCTA 1260
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Db  1201 AGTCCTCGGGCGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCCTGCGTCTGGTGGTGGTGGACATCCTA 1260

Qy  1261 GCCCTGGGTTTTTGGGCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTCGTGTCAGATGAGA 1320
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Db  1261 GCCCTGGGTTTTTGGGCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTCGTGTCAGATGAGA 1320

Qy  1321 AGGCAGCACAGAGAGGCGGAACCAAAGGGGGTGTGAGCGTACCGGCCCCAGCAGAGGTAGCCGAG 1380
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Db  1321 AGGCAGCACAGAGAGGCGGAACCAAAGGGGGTGTGAGCGTACCGGCCCCAGCAGAGGTAGCCGAG 1380

Qy  1381 ACTGGAGCCCTAGAGGCTGGATCTTGGAGAAATGAGAAGCCAGAGGCCATCTGAGGG 1440
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Qy  1441 GGAGCCGGGTAACTGTCCTGCTCATTAGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Db  1441 GGAGCCGGGTAACTGTCCTGCTCATTAGCCACTTCCTTTTAACTGCCAAGAAATT 1500

Qy  1501 TTTTAAAATAAAATATTTTATAAT 1522
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Db  1501 TTTTAAAATAAAATATTTTATAAT 1522
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RESULT 7
LOCUS           AR171392                1522 bp    DNA        linear    PAT 17-DEC-2001
DEFINITION      Sequence 1 from patent US 6297041.
ACCESSION       AR171392
VERSION         AR171392.1  GI:17910342
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 1522)
  AUTHORS       Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE         MN Gene and protein
  JOURNAL       Patent: US 6297041-A 1 02-OCT-2001;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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ORIGIN
Query Match    100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 ACAGTCAGCCGACCGATGGGCTCCCCTGTGCCCCAGCCTCCCCTCTCCTTCTGTTGATCCCGGCC 60
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Db      1 ACAGTCAGCCGACCGATGGGCTCCCCTGTGCCCCAGCCTCCCCTCTCCTTCTGTTGATCCCGGCC 60

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGCGTCGTCACTGCGTTCTGATGCCTGTCAT 120
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Db     61 CCTGCTCCAGGCCTCACTGTGCAACTGCGTCGTCACTGCGTTCTGATGCCTGTCAT 120

Qy    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGAATTCCCCCTTGGGAGGCGCTTCTTCTGGGGGAA 180
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Qy    241 CCACCCCGGAGAGGAGGATCTACCTGGAGGAGGATCTGGAGAGGAGGAGGAGGAGGATCTACCT 300
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Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
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Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420

Qy    421 GACCAGAGTCATTGGCGCGGTCTATGGAGGGCGACCCCGCCGGGGTGTCCCCAGCCTGC 480
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Qy    481 GCGGGGCCGCCGCTTCCAGTCCCCGGTGGAATATCCGCCCCCTTCTCCGCCCCGGCC 540
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Db    481 GCGGGGCCGCCGCTTCCAGTCCCCGGTGGAATATCCGCCCCCTTCTCCGCCCCGGCC 540

Qy    541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCAGAACTGGCGCCCTGCGC 600
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Db    541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCAGAACTGGCGCCCTGCGC 600

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCGGGGTCCC 660
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Db    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCGGGGTCCC 660

Qy    661 GGGCGCGGGAGTACCGGGCTCTGCAGCTGCAGCTGCAGGTCGTTCCGGGC 720
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Qy    721 TCGGAGCACACTGTGGGAGAGGCCACCCGTTTCCCTGCCGAGGATCCAGGTGGTTCACCTCAGC 780
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Qy    781 ACCGGCCTTTGCCAGAGTTGACGAGGCCGTTGGGGCGGCCCCGGGAGGGCCTGGCGTGTTGGCC 840
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Db    781 ACCGGCCTTTGCCAGAGTTGACGAGGCCGTTGGGGCGGCCCCGGGAGGGCCTGGCGTGTTGGCC 840

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Db    841 GCCTTTCTGGAGGACGGGCCCCGGAGAAAAACAGTGCCTATGGCTTGCTGTCTGTCTGCGCTG 900

Qy    901 GAAGAAATCGGCTGGAGGAAGGCTCAGAGACTCAGAGTCCCAGGGACTGGACATTATCTGCACTC 960
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Db    961 CTGCCCTCTGACTTCAGCGCCGCTACTTCCAATATGAGGGGGTCTTCTGACTACACACCCGCCTGT 1020

Qy   1021 GCCCAGGGGGTGTCATCTGGACTGTGTTTTAACCAGACACAGTGAATGCGAGTGCTGAAGCAGCTC 1080
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Db   1021 GCCCAGGGGGTGTCATCTGGACTGTGTTTTAACCAGACACAGTGAATGCGAGTGCTGAAGCAGCTC 1080

Qy   1081 CACACCCTCTCTGACACCCCTGTGGGGGACCTGGTCGACTCTCGGGCTACAGCTGAACTTCCGA 1140
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Db   1081 CACACCCTCTCTGACACCCCTGTGGGGGACCTGGTCGACTCTCGGGCTACAGCTGAACTTCCGA 1140

Qy   1141 GCGACGGCAGCCTTTGAAATGGGCAGAGTGATTGAGGGCCTCCTTCCCTGCTGGAAGTGGACAGC 1200
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Db   1141 GCGACGGCAGCCTTTGAAATGGGCAGAGTGATTGAGGGCCTCCTTCCCTGCTGGAAGTGGACAGC 1200

Qy   1201 AGTCCTCGGGCTGCTGAGCCAGTCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260
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Db   1201 AGTCCTCGGGCTGCTGAGCCAGTCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTGCACCAGCGTGCGGGTTCCTTGCTGCTGGAGATGAGA 1320
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Db   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTGCACCAGCGTGCGGGTTCCTTGCTGCTGGAGATGAGA 1320

Qy   1321 AGGCAGCACAGAAGGGGACCAAAGGGGGTGTGAGCTACCGGCCACAGCAGAGGTAGCCGAG 1380
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Qy   1441 GGAGCCGGTAACTGTCCCTGTCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
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Db   1441 GGAGCCGGTAACTGTCCCTGTCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500

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Db   1501 TTTTAAAATAAATATTTATAT 1522
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LOCUS           AR171563                1522 bp    DNA        linear    PAT 17-DEC-2001
DEFINITION      Sequence 1 from patent US 6297051.
ACCESSION       AR171563
VERSION         AR171563.1  GI:17910513
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 1522)
  AUTHORS       Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE         MN Gene and protein
  JOURNAL       Patent: US 6297051-A 1 02-OCT-2001;
FEATURES             Location/Qualifiers
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Query Match             100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     61 CCTGCTCCAGGCCCTCACTGTGCAAACTGCTGCTCGTCAGCCCCAGCCCTGGTGCCTCCAT 120
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Db     61 CCTGCTCCAGGCCCTCACTGTGCAAACTGCTGCTCGTCAGCCCCAGCCCTGGTGCCTCCAT 120

Qy    121 CCCCAGAGAGTTGCCCCGATGCAGGAGTGAGCAGCCTTCCCCTTGGGAGGAGGAGGAGGAA 180
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Qy    181 GATGACCCACTGTGGGCGAGGAGGATCTGCCCAGTGAAGAGGGCTTCTCTGTGTCCATGGA 240
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Qy    301 GAAGTTAAGCCTAAATCAGGAGAAGAGGAGGGCTCCCTGAAGTTAGAGTTAGAGGATCTACTACTGTT 360
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Db    301 GAAGTTAAGCCTAAATCAGGAGAAGAGGAGGGCTCCCTGAAGTTAGAGTTAGAGGATCTACTACTGTT 360

Qy    361 GAGGCTCCTGGAGGAGGATCTCAAGAGGACCCCAGAGAATAAATGCCCACAGGGACAAAGAAGAGGGAT 420
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Db    361 GAGGCTCCTGGAGGAGGATCTCAAGAGGACCCCAGAGAATAAATGCCCACAGGGACAAAGAAGAGGGAT 420

Qy    421 GACCAGAGTCATTGGGCGCTATGGAGGGGACCCCGCCCCGGGGTGTCCCCAGCCTGC 480
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Qy    481 GCGGGGCCGCTTCCAGTCCCCGGTGGGATATCCGCCCGGGCCGCTTCTCTGCCCAGCTGC 540
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Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCCTCGGGCCTAGAGATGGCTCTGGAGTCCC 660
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Qy    661 GGGCCGGGAGTACCGGGGCTCTGCAGCTGCATCCACTCGGCGTCGCAGGTCGTCCCGGGC 720
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Db    661 GGGCCGGGAGTACCGGGGCTCTGCAGCTGCATCCACTCGGCGTCGCAGGTCGTCCCGGGC 720

Qy    721 TCGGAGCACACTGTGGAAGGCCACACGTTTCCCTGCCAGATCCACCGTCACCTCAGC 780
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Db    721 TCGGAGCACACTGTGGAAGGCCACACGTTTCCCTGCCAGATCCACCGTCACCTCAGC 780

Qy    781 ACCGGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGGAGGGCCCTGGCCGTGGTTCGGGCC 840
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Db    781 ACCGGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGGAGGGCCCTGGCCGTGGTTCGGGCC 840

Qy    841 GCCTTTCTTGGGAGGAGGAGGCTCAGGGAGAAGAAAACAGTGCCTTATGAGCCAGTTGCTCTGCTCG 900
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Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCCTGCACTC 960
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Qy    961 CTGGCCCTCCTGACTTCAGCCGCGCTACTTCCAATATGAGGGGGTCTCTGACTTACCGCCGTGT 1020
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Db    961 CTGGCCCTCCTGACTTCAGCCGCGCTACTTCCAATATGAGGGGGTCTCTGACTTACCGCCGTGT 1020

Qy   1021 GCCCAGGGTGTCATCTGACTGTGTGTTTAACCAGACAGTGATTGCTAAGCAGCTC 1080
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Qy   1081 CACACCCTCTCTGACACCCCTGTGGGGGACCTGGTTGACTCTGGGCTTGGGCTACAGCTGAACTTCCGA 1140
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Qy   1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTCGCGCGTGCGTGCGTGCGTGGACATTCCTA 1260
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Qy   1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGTCACCAGCGGTCGGTTCCTTGTTGTGCAGATGAGA 1320
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Db   1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGTCACCAGCGGTCGGTTCCTTGTTGTGCAGATGAGA 1320

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTGGAGCTACCGGCCGCCAGCAGGAGGTAGCCGAG 1380
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Qy   1381 ACTGGAGCCTAGGACCCGATCTTGGGAGAAATGTGAGAAGGCCAGCCAGAGGCCATCTGACGGG 1440
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Qy   1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Db   1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500

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RESULT 9
BD243152

LOCUS   BD243152   1522 bp   DNA   linear   PAT 17-JUL-2003
DEFINITION MN gene and protein.
ACCESSION   BD243152
VERSION   BD243152.1 GI:33052922
KEYWORDS   JP 2002528085-A/1.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 1 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT   OS   Homo sapiens (human)
            PN   JP 2002528085-A/1
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 200057845
            PR   23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
            JAN ZAVADA, SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
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            FH   Key   Location/Qualifiers
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Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCCACAGGACAAAAGAGGGGAT 420
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Qy      661 GGGCGGGAGTACCGGGCGCTTCTGCAGCTGGCCAGGTCGTTCCGGGC 720
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Qy      841 GCCTTTCTGGAGGAGGGCCCGGAGAGAAAACAGTGCCTATGAGCAGTTGCTGCTGC 900
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Qy     1081 CACACCCTCTTCTGACACCCTGTGGGGACCGGTTGACTCTGGGTTACAGCTGAACTTCCGA 1140
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Qy     1201 AGTCCTTCGGCGTGCTGAGCCGCAGTCCAGCCTGAGCTGAATTCCCCTGGCTGGACATCCTA 1260
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Qy     1381 ACTGGAGGCCTAGAGCGCTGGAGATCTTGGAGAATGTGAGAAGCCTACCGGCACCATCTGAGGG 1440
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Qy     1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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RESULT 10

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ACCESSION   CQ834035
VERSION     CQ834035.1  GI:50833640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Astle,J.H., Boardman,L.A., Bugart,L.J., Burgess,C.C., Catino,T.J.,
            Dwived,P., Huntress,M., Johnson,K.A., Lewis,M.E., Maimonis,P.J.,
            Myerow,S.H., Brown-Shimer,S.L., Thiagalingam,A., Thibodeau,S.N. and
            Molino,G.A.
  TITLE     Detection methods using TIMP 1 for colon cancer diagnosis
  JOURNAL   Patent: EP 1439393-A 71 21-JUL-2004;
            Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
            AND RESEARCH (US)
FEATURES             Location/Qualifiers
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Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy   241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
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Qy   301 GAAGTTAAGGCCTAAATCAGAAGAAGAGAAGGGTCCCTGAAGTTAGAGGATCTACCTACTTGTT 360
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Qy   781 ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCGCCTGCCCGGTTGCACTCAGC 840
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Db   931 GAAGAAATCGCTGAGGAAGGCTCAGGTCCAGGACTGGACAGTACATATCTGCACTC 990

Qy   961 CTGCCCTCTGACTTCAGCTCATCTGACACAGTGAATGTGAGTGCTCAAGCAGTC 1020
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Db   991 CTGCCCTCTGACTTCAGCTCATCTGACACAGTGAATGTGAGTGCTCAAGCAGTC 1050

Qy  1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACAGTGATGTGCTAAAGCAGTC 1080
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Qy  1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGTGTGAGCGTAGCCGGGTAGCCGAG 1380
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Db  1351 AGGCAGCACAGAAGGGGAACCAAAAGGGGTGTGAGCGTACCGGGTAGCCGAG 1410

Qy  1381 ACTGGAGCCTAGACGGCTGGATCTTGGAGAATGTGAGAGCCAGCGCATCTGAGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1411 ACTGGAGCCTAGACGGCTGGATCTTGGAGAATGTGAGAACCAGCCATCTGAGGG 1470

Qy  1441 GGAGCCGGGTGAACTGTCCTGTGCTCATTATGGCCACTTCCTTTTAACTGCCAAGAAAATT 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1471 GGACCGGGTTAACTGTCCTGTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAAATT 1530

Qy  1501 TTTTAAAAATAAAATATTTATAAT 1522
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Db  1531 TTTTAAAAATAAAATATTTATAAT 1552
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RESULT 11
AX330007

LOCUS       AX330007                1552 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 516 from Patent WO0194629.
ACCESSION   AX330007
VERSION     AX330007.1  GI:18102985
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 516 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..1552
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy     1 ACAGTCAGCGCCAATGGCTCCCCCTGTGCCCCCAGCCCCTGGCCTCCCTCTCGTTGAATCCCGGCC 60
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Db    31 ACAGTCAGCGCCAATGGCTCCCCCTGTGCCCCCAGCCCCTGGCCTCCCTCTCGTTGAATCCCGGCC 90

Qy    61 CCTGCTCCAGGCCTCACTGTGCCACTGCTGTCGCTTCTGATGCCTGCATG 120
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Db    91 CCTGCTCCAGGCCTCACTGTGCCACTGCTGTCGCTTCTGATGCCTGCATG 150

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
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Db   151 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 210

Qy   181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGAGGATTCACCCAGAGGAGGAT 240
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Qy     211 GATGACCCACTGGGCGAGGAGGATTCACCCAGTGAAGAGGAGGAT 270

Qy     241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
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Db    1351 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 1410

Qy     271 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 330

Qy     301 GAAGTTAAGGCCTAAATCAGAGAAGAGAGAGGGGTCCCTGAAGTTAGAGGACTACCTACTGTT 360
Db    1411 ACTGGAGAGCCTTAGAGCGGAGGCTGGATCTTGGAGAATGTGAGAAGGCCAGCCAGCAGAGGCATCTGAGGG 1470

Qy     331 GAAGTTAAGGCCTAAATCAGAGAAGAGAGAGGGGTCCCTGAAGTTAGAGG 390

Qy     361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCAGATAATGC 420
Db    1471 GGAGCGCGGGTAACTGTCCCTGCTCATTATGCCACTTCCTTTTAAACTGCCAAGAAAATT 1530

Qy     391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCAGAT 450

Qy     421 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCGCCCTGGCCCTGGCCTGC 480
Db    1531 TTTTAAAAATAAAATATTTTATAAT 1552

Qy     451 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCGCCCTGGCCCTGG 510

Qy     481 GCGGGGCCGGCTTCAGTCCCCGGTGGGATATCCGCCCCGCCCAGCTGCGCCGCCTTCTGCCCGCC 540

Qy     511 GCGGGGCCGGCTTCCAGTCCCCGGTGGGATATCCGCCCGCCCAGCTGCGCCGCCTTCTGCCCGCC 570

Qy     541 CTGCGCGCCCCCTGGGAACTCCTCGGGCTTCCAGCGTCCCGGCTCCCGGCTCCCG 600

Qy     571 CTGCGCGCCCCCTGGGAACTCCTCGGGCTTCCAGCGTCCCGGCTCCCG 630

Qy     601 AACAATGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC 660

Qy     631 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC 690

Qy     661 GGGCGGGGAGTACCGGGGCTTCAGCTGCCATCTCGACTCTGGGGGCGTCGGCGTGCTGCAGGTCGTCGCCGGGC 720

Qy     691 GGGCGGGGAGTACCGGGGCTTCAGCTGCCATCTCGACTCTGGGGGCGTCGGC 750

Qy     721 TCGGAGGCACAGTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAACGTGGTTCACCTCAGC 780

Qy     751 TCGGAGGCACAGTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAAC 810

Qy     781 ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840

Qy     811 ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGGCGCCCGGGAGG 870

Qy     841 GCCTTTCTGGAGGAGGGGCCCCGGAAGAAAAACAGTGCCATTGAGCAGTTGCTGTCTCGCTTG 900

Qy     871 GCCTTTCTGGAGGAGGGGCCCCGGAAGAAAAACAGTGCCATTGAGCAGTTGCTGTCTCGCTTG 930

Qy     901 GAAGAGAAATCGCTGAGGAAGGCTCAGGAGGGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy     931 GAAGAGAAATCGCTGAGGAAGGCTCAGGAGGGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990

Qy     961 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTTCTCTGACTCCACCGCCCGTGT 1020

Qy     991 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTTCTCTGACTCCACCGCCCGTGT 1050

Qy    1021 GCCCAGAGGGTGTCATCGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080

Qy    1051 GCCCAGGGTGTCATCGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1110

Qy    1081 CACACCCCTCTCTGACACCCTGTGGGACTGGTCGTGACTCTCGGGCTACAGCTGAACTTCCGA 1140

Qy    1111 CACACCCCTCTCTGACACCCTGTGGGACTGGTCGTGACTCTCGGGCTACAGCTGAACTTCCGA 1170

Qy    1141 GCCACGCAGCCCTTTGAATGGGGCCAGTGATTGAGGCCTCCTTCCTTTCCCTGGCGTGGCACAGC 1200

Qy    1171 GCCACGCAGCCCTTTGAATGGGGCCAGTGATTGAGGCCTCCTTCCTTTCCCTGGCGTGGCACAGC 1230

Qy    1201 AGTCCTCGGGCTGCTGAGCCAGTCATCCAGCTGAATTCTCGCCTGCGCTGCTGCTGGCTGCATCCTA 1260

Qy    1231 AGTCCTCGGGCTGCTGAGCCAGTCATCCAGCTGAATTCTCGCCTGCGCTGCTGGCTGCATCCTA 1290

Qy    1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCAGCGTCGGCGTTCCTTGTGTGCAGGATGAGA 1320

Qy    1291 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCAGCGTCGGCGTTCCTTGTGTGCAGGATGAGA 1350
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Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 1522;  Conservative  0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy       1 ACAGTCAGCCGCATGGCTCCCCGTGCCCCAGCACCCTGGCTCCCTCGTTGTGATCCCGGCC 60
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Db      31 ACAGTCAGCCGCATGGCTCCCCGTGCCCCAGCCACCCTGGCTCCCTCGTTGTGATCCCGGCC 90

Qy      61 CCTGCTCCAGGCCCTCACTGTCGAACTGCTGCTGCTTCGTTCGATGGCCCATCCCAT 120
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Db      91 CCTGCTCCAGGCCCTCACTGTCGAACTGCTGCTGCTTCGTTCGATGGCCCATCCCAT 150

Qy     121 CCCCAGAGGTTGCCCCGGATGCAGGAGAGGGATTCCCCTGGGAGGCTCTTCTGGGGAA 180
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Db     151 CCCCAGAGGTTGCCCCGGATGCAGGAGAGGGATTCCCCTGGGAGGCTCTTCTGGGGAA 210

Qy     181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGAGGATCACCCAGAGAGGAT 240
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Db     211 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGAGGATCACCCAGAGAGGAT 270

Qy     241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
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Db     271 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 330

Qy     301 GAAGTTAAGGCCTAAATCAGAGAAGAGAGAGGGGTCCCTGAAGTTAGAGGACTACTGTT 360
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Db     331 GAAGTTAAGGCCTAAATCAGAGAAGAGAGAGGGGTCCCTGAAGTTAGAGGACTACTGTT 390

Qy     361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
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Db     391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
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RESULT 13
LOCUS       AX333244                1552 bp    DNA        linear   PAT 09-JAN-2002
DEFINITION  AX333244 Sequence 3753 from Patent WO0194629.
ACCESSION   AX333244
VERSION     AX333244.1  GI:18123878
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE       Cancer gene determination and therapeutic screening using signature
            gene sets
JOURNAL     Patent: WO 0194629-A 3753 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..1552
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match     100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         1 ACAGTCAGCCGCAlTGGCTCCCCCGTGCCCCCAGCCCGCTCCCTCTGTTGATCCGGCC 60
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Db        31 ACAGTCAGCCGCAlTGGCTCCCCCGTGCCCCCAGCCCGCTCCCTCTGTTGATCCGGCC 90

Qy        61 CCTTGCTCCAGGCCTCACTGTGCTGCAACTGCTGCTGCTGCTTCGATGCCTTGTGCCAT 120
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Db        91 CCTTGCTCCAGGCCTCACTGTGCTGCAACTGCTGCTGCTTCGATGCCTTGTGCCAT 150

Qy       121 CCCCAGAGGTTGCCCCGGATGCGAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
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Db       151 CCCCAGAGGTTGCCCCGGATGCGAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 210

Qy       181 GATGAGACCCAGTGGGCGACGAGGAGAGGATTCTGCCCAGTGAAGAGGATCCAGAGAGGAT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       211 GATGAGACCCAGTGGGCGACGAGGAGAGGATTCTGCCCAGTGAAGAGGATCCAGAGAGGAT 270

Qy       241 CCACCCGAGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCT 300
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Db       271 CCACCCGAGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCT 330

Qy       301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       331 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy       361 GAGGCTCCTGGAGATCCTCAAGGAACCCCCAGAGAATAAATGCCCACAGGAGACAAAAGAAGGGGAT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       391 GAGGCTCCTGGAGATCCTCAAGGAACCCCCAGAGAATAAATGCCCACAGGAGACAAAAGAAGGGGAT 450

Qy       421 GACCAGAGTCATTGGGCGCTAlTGGAGGGCCACCCGGCCCTGGCCGCCCGGGGTGTCCCCAGCCTGC 480
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Db       451 GACCAGAGTCATTGGGCGCTAlTGGAGGGCCACCCGGCCCTGGCCGCCCGGGGTGTCCCCAGCCTGC 510

Qy       481 GCGGGGCCGCTTCCAGTCCCCGGTGGATATCCGGCCCAGCTCGCCGCCCTTCTGCCCGGCC 540
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Qy       541 CTGCGCGCCCCCTGGAACTCCTGGGCTTCCCAGCTTCCCAGCTCCCGCCGCCCTGCGC 600
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RESULT 14
LOCUS        AX336174        1552 bp    DNA    linear    PAT 09-JAN-2002
DEFINITION   Sequence 6683 from Patent WO0194629.
ACCESSION    AX336174
VERSION      AX336174.1  GI:18126893
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Young,P.B., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
             Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE      Cancer gene determination and therapeutic screening using signature
             gene sets
  JOURNAL    Patent: WO 0194629-A 6683 13-DEC-2001;
             Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..1552
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                     /mol_type="unassigned DNA"
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ORIGIN
Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
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Db         31 ACAGTCAGCCGCATGGCTCCCCGTGTGCCCCAGCCCCTGCTCCCTCTCGTTGGATCCCGCC 90

Qy         61 CCTGCTCCAGGCCCTCACTGTGCACTGCTGCTTCTGCTTGATGCCTTCCAT 120
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Db         91 CCTGCTCCAGGCCCTCACTGTGCACTGCTGCTTCTGCTTGATGCCTTCCAT 150

Qy        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCCTTGGGGAGGGCCTCTTTCTGGGGAA 180
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Db        151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCCTTGGGGAGGGCCTCTTTCTGGGGAA 210

Qy        181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGAGGAATCACCCAGAGAGGAGGAT 240
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Db        211 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGAGGAATCACCCAGAGAGGAGGAT 270

Qy        241 CCACCCCGGAGAGGAGGGATTCTACCTGGAGAGGAGGATCTACCT 300
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Db        271 CCACCCCGGAGAGGAGGGATTCTACCTGGAGAGGAGGATCTACCT 330

Qy        301 GAAGTTAAGGCCTAAATCAGAGAGAGAGAGGGGCTTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GAAGTTAAGGCCTAAATCAGAGAGAGAGAGGGGCTTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy        361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAAGTGCCCACAGGACAAAGAAAGGAAGGGGAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAAGTGCCCACAGGACAAAGAAAGGAAGGGGAT 450

Qy        421 GACCAGAGTCATTGGCGCTATGGGAGGGGAGGCGCGCGCGCCCGGGTGTCCCCAGCCGCTGC 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        511 GCGGGGCCCGCGTTCCCGGGTGGAATATCGGCGGGCCGCGCCTTCGGGGCC 570

Qy        541 CTGCGCCCCTGGAACTCCCTGGGCTTCCAGCTCCCGCGCCTCGCCCTTCGGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTGCGCCCCTGGAACTCCCTGGGCTTCCAGCTCCCGCGCCTCGCCCTTCGGC 630

Qy        601 AACAATGGCCACACTGTGCAAACTGACCCCTGCCTCCCTGGGCTAGAGATGGCTCTGGGTCC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 AACAATGGCCACACTGTGCAAACTGACCCCTGCCTCCCTGGGCTAGAGATGGCTCTGGGTCC 690

Qy        661 GGGCGGGAGTACCCGGGCTCTGCGACTGCACTGCACTGCGCACTGCTCGTCCGGGC 720
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Db        691 GGGCGGGAGTACCCGGGCTCTGCGACTGCACTGCACTGCGCACTGCTCGTCCGGGC 750

Qy        721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCTCAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCTCAGC 780
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Db    751 TCCGAGCACTGTGGAAGGCCACCGGTTTCCTGCCGAGATCCACGTGGTTCACCTCAGC  810
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Qy    781 ACCGCCTTTGCCAGAGTTGACGAGCGGCCCTTGGGCGGCCGGCCGGTGTTGGCC  840
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Db    811 ACCGCCTTTGCCAGAGTTGACGAGAGGCCCTTGGGGCGGCCGGCCGGTGTTGGCC  870
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 GCCTTTCTGGAGGAGGGCCCGGAGAAAACAGTGCCTATGAGCAGTGCCTCTCGCTTG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTCTGGAGGAGGGCCCGGAGAAAACAGTGCCTATGAGCAGTGCCTCTCGCTTG  930
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC  990
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Qy    961 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATCAGAGGGTCTCTTGACTACACCGCC  1020
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Db    991 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATCAGAGGGTCTCTTGACTACACCGCC  1050
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Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC  1080
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Db   1051 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC  1110
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Qy   1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGGTAGACTCTCGGTTCAGCTGAACTTCCGA  1140
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Db   1111 CACACCCTCTCTGACACCCTGTGGGGACCTGGGTAGACTCTCGGTTCAGCTGAACTTCCGA  1170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 GCCACGCAGCCCTTGAATGGGCGAGTGATTGAATGGGCCAGTGTTCAACTTGAGGGACAGC  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 GGCACGCAGCCCTTTGAATGGGCGAGTGATTGAGTGGGCCTCCAGTGTTCGAGTGGACAGC  1230
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Qy   1201 AGTCCCTCGGGCTGCTGAGCCAGTCAGCTGAATTCCTGCCTCGTCGTGTGGTGCATCCTA  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 AGTCCCTCGGGCTGCTGAGCCAGTCAGCTGAATTCCTGCCTCGTCGTGTGGTGCATCCTA  1290
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Qy   1261 GCCCTGGTTTTTGGCCTCCTTTTGGCTCGTGTCACCAGGCGTCGGTTCGTTGCAGATGAGA  1320
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Db   1291 GCCCTGGTTTTTGGCCTCCTTTTGGCTCGTGTCACCAGGCGTCGGTTCGTTGCAGATGAGA  1350
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Qy   1321 AGGCAGCACAGGAGGGGGACCAAAGGGGGGTGTGAGCTACCAGCGCAGAGGTAGCCGAG  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AGGCAGCACAGGAGGGGGACCAAAGGGGGGTGTGAGCTACCAGCGCAGAGGTAGCCGAG  1410
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Qy   1381 ACTGGGACGCCTAGAGGCTGGATCTTCTTGGAGAATGTGAGAAGGCTAGGGGG  1440
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Db   1411 ACTGGGACGCCTAGAGGCTGGATCTTCTTGGAGAATGTGAGAAGGCATCTGACGG  1470
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Qy   1441 GGAGCCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT  1500
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Db   1471 GGAGCCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT  1530
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Qy   1501 TTTTAAAATAAAATATTTTATAAT  1522
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Db   1531 TTTTAAAATAAAATATTTTATAAT  1552
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REFERENCE   2 (bases 1 to 1552)
  AUTHORS   Pastorek,J., Pastorekova,S., Callebaut,I., Mornon,J., Zelnik,V.,
            Opavsky,R., Zatovicova,M., Liao,S., Portetelle,D., Stanbridge,E.J.,
            Zavada,J. and Burny,A.
  TITLE   Cloning and characterization of MN, a human tumor-associated
            protein with a domain homologous to carbonic anhydrase and a
            putative helix-loop-helix DNA binding segment
  JOURNAL   Oncogene 9 (10), 2877-2888 (1994)
  MEDLINE   94367034
   PUBMED   8084592
REFERENCE   3 (bases 1 to 1552)
  AUTHORS   Pastorek,J.
  TITLE   Direct Submission
  JOURNAL   Submitted (19-JUL-1994) J. Pastorek, Institute of Virology, Slovak
            Academy of Sciences, Dubravska 9, 842 46 Bratislavia, SLOVAK
            REPUBLIC
  REMARK   revised by [4] MAT
REFERENCE   4 (bases 1 to 1552)
  AUTHORS   Pastorek,J.
  TITLE   Direct Submission
  JOURNAL   Submitted (28-SEP-1995) J. Pastorek, Institute of Virology, Slovak
            Academy of Sciences, Dubravska 9, 842 46 Bratislavia, SLOVAK
            REPUBLIC

COMMENT   On Sep 29, 1995 this sequence version replaced gi:558593.
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ORIGIN

Query Match   100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
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Job time : 6359 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: February 6, 2005, 04:09:04

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Perfect score: 1522
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Searched: 4134886 seqs, 2624710521 residues
Scoring table: OLIGO_NUC
Word size :   50
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Total number of hits satisfying chosen parameters: 68
Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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DT   19-AUG-1996 (first entry)
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KW   neoplastic; pre-neoplastic; disease; antisense therapy; antibody;
KW   vaccine; vertebrate; immunisation; ss.
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PF   15-JUN-1995; 95WO-US007628.
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PR   07-JUN-1995; 95US-00477504.
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PR   07-JUN-1995; 95US-00485049.
PR   07-JUN-1995; 95US-00485864.
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PA   (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA   (VIRO-) INST VIROLOGY.
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PI   Zavada J, Pastorekova S, Pastorek J;
XX
DR   WPI; 1996-049679/05.
DR   P-PSDB; AAR88058.

XX
PT   MN gene, protein and nucleic acid fragments - used as primers and probes
PT   in the detection of MN antigens and antibodies, and in the treatment of
PT   (pre)neoplastic disease.
XX
PS   Claim 1; Fig 1; 102pp; English.
XX
CC
CC   The present sequence is the full length MuTu endogenous cellular
CC   component, MN, cDNA clone, which was isolated from lymphocytic
CC   choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV, the
CC   exogenous MuTu transmissible agent (MX), infection increases the
CC   expression level of the MN gene. MN is a putative oncogene, and can
CC   therefore be used in the development of prods. for the diagnosis and
CC   treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC   treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC   antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC   vaccine contg. immunogenic amounts of the MN protein can be used to
CC   immunise a vertebrate against a NP disease associated with MN antigen
CC   expression. (Updated on 25-MAR-2003 to correct PR field.)
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Query Match   100.0%;   Score 1522;   DB 2;   Length 1522;
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RESULT 2
AAA16540
ID   AAA16540 standard; cDNA; 1522 BP.
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DT   16-JUN-2000 (first entry)
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KW   Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW   oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW   MN/CA IX isoenzyme; db.
XX
OS   Homo sapiens.

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PN   US6027887-A.
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XX
PR   21-OCT-1992;   92US-00964589.
PR   30-DEC-1993;   93US-00177093.
PR   15-JUN-1994;   94US-00260190.
PR   07-JUN-1995;   95US-00477504.
PR   07-JUN-1995;   95US-00481658.
PR   07-JUN-1995;   95US-00485049.
PR   07-JUN-1995;   95US-00485862.
PR   07-JUN-1995;   95US-00485863.
PR   07-JUN-1995;   95US-00486756.
PR   07-JUN-1995;   95US-00487077.
XX
PA   (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI   Pastorek J,  Zavada J,  Pastorekova S;
XX
DR   WPI; 2000-194827/17.
DR   P-PSDB; AAY53228.
XX
PT   Nucleic acid based assay for diagnosing a wide variety of
PT   preneoplastic/neoplastic disease comprises screening for the presence of
PT   abnormal MN gene expression in a vertebrate.
XX
PS   Claim 1; Fig 1; 87pp; English.
XX
CC   The present invention describes a method of screening for
CC   preneoplastic/neoplastic disease. The method comprises: (1) determining
CC   whether abnormal MN gene expression is present in a vertebrate; and (2)
CC   if abnormal MN gene expression is determined to be present in the
CC   vertebrate, determining that the vertebrate has a significant risk of
CC   having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC   encodes an MN protein (also refered to as MN/CA IX isoenzyme). The MN
CC   protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC   is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC   in a vertebrate, preferably a human. The disease detected is mammary,
CC   bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC   vaginal, vulval, prostate, liver, lung, thyroid, pancreatic,
CC   testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC   duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC   mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC   mucosa, pancreatic duct epithelium or liver duct epithelium
CC   preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC   AAY53245 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
```

```
Query Match             100.0%;  Score 1522;  DB 3;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522; Conservative   0; Mismatches  0; Indels  0; Gaps  0;
```

```
Qy        1 ACAGTCAGCGCGCATGGCTCCCCCCGTGCCCCAGCCGTCCCCTTCCTGCTCGTTGGATCCCCGGCC     60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ACAGTCAGCGCATGGCTCCCCCCGTGCCCCAGCCGTCCCCTTCCTGCTCGTTGGATCCCCGGCC     60

Qy       61 CCTGCTCCAGGGCCTCACTGTGTGCAACTGTCGTCCACTGTCCACTGCTGCTTTCTGATGCCTGTCCAT    120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CCTGCTCCAGGGCCTCACTGTGTGCAACTGTCGTCCACTGTCCACTGCTGCTTTCTGATGCCTGTCCAT    120

Qy      121 CCCCAGAGGGTTGCCCCGGATGCAGGAGGGATTCCCCCTTGGGAGGAGAGGCTCTTCTGGGGAA    180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CCCCAGAGGGTTGCCCCCGGATGCAGGAGGAATTCCCCCTTGGGAGGAGAGGCTCTTCTGGGGAA    180

Qy      181 GATGACCCACTCGGCGAGGAGGAGGATCTGCCCAGTGAAGAGGAGGAGGATTCACCCAGAGAGGAGGAT    240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GATGACCCACTCGGCGAGGAGGAGGATCTGCCCAGTGAAGAGGAGGAGGATTCACCCAGAGAGGAGGAT    240

Qy      241 CCACCCCGGAGGAGGAGGAGGATCTTACCTGGAGGAGGATCTACCT    300
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Db      241 CCACCCCGGAGGAGGAGGAGGATCTTACCTGGAGGAGGATCTACCT    300

Qy      301 GAAGGTTAAGCCTAAAATCAGAAGAAGAGAGGGGCTTCCCTGAAGGTTAGAGAGGATCTACCTGTT    360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GAAGGTTAAGCCTAAAATCAGAAGAAGAGAGGGGCTTCCCTGAAGGTTAGAGAGGATCTACCTGTT    360

Qy      361 GAGGGCTTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGGACAAAGAAGGATC    420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAGGGCTTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGGACAAAGAAGGATC    420

Qy      421 GACCAGAGTCATTGGCGCTATGGAGAGGCGACCCGGCCCCGGGGGTGTCCCCAGCCTGC    480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GACCAGAGTCATTGGCGCTATGGAGAGGCGACCCGGCCCCGGGGGTGTCCCCAGCCTGC    480

Qy      481 GCGGGCGGCGCTTCCAGTCCCCGGTGGAATATCCGGCCGCCCCCAGCTGCGCCCGGCC    540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCGGGCGGCGCTTCCAGTCCCCGGTGGAATATCCGGCCGCCCCCAGCTGCGCCCGGCC    540

Qy      541 CTGCCCCCCTGGGACTCCCTGGAGCTTCCAGCTCCCGCCGCGCCCCCAGCTGCGCC    600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CTGCCCCCCTGGGACTCCCTGGAGCTTCCAGCTCCCGCCGCGCCCCCAGCTGCGCC    600

Qy      601 AACAATGGGCACACAGTGTGCAACTGACCCCTCGCCTCTTCGGCTGAGAGATGGCTCTCTGGGTCCC    660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACAATGGGCACACAGTGTGCAACTGACCCCTCGCCTCTTCGGCTGAGAGATGGCTCTCTGGGTCCC    660

Qy      661 GGGGCGGGGAGTACCGGGGCTTGCAGTCGCATCTGCACTGGGGGGGTGCAGTTGCGTCCGGGC    720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGGGCGGGGAGTACCGGGGCTTGCAGTCGCATCTGCACTGGGGGGGTGCAGTTGCGTCCGGGC    720

Qy      721 TCGGAGCACACTGTGGAGGCCACCCGTTTCCCTGCCGAGATCCAGTGGGTTCACCTCAGC    780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TCGGAGCACACTGTGGAAGGCCACCCGTTTCCCTGCCGAGATCCAGTGGGTTCACCTCAGC    780

Qy      781 ACCGGCCTTTGCCGAGAGTTGACGAGGCCGTTGGGGCGCCCCGGGGAGGGCCTGTGTTGGCC    840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 ACCGGCCTTTGCCGAGAGTTGACGAGGCCGTTGGGGCGCCCCGGGGAGGGCCTGTGTTGGCC    840

Qy      841 GCCTTTCTGGAGGAGGGGCCCGGAAAAACAGTGGCCTATGAGCAGTTGCTGTTGCTGCCTTG    900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GCCTTTCTGGAGGAGGGGCCCGGAGAAAAACAGTGGCCTATGAGCAGTTGCTGTGTGCTGCCTTG    900

Qy      901 GAAGGAAATCGCTGAGGAAGGCTCAGGATCCCAGGACTGGACAGTATCTGCACTC    960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GAAGGAAATCGCTGAGGAAGGCTCAGGAGGACTCAGGGAGGACTGGACACATATCTGCAACTC    960

Qy      961 CTGCCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT    1020
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Db      961 CTGCCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT    1020

Qy     1021 GCCCAGGGGTGTCAATCTGGACTGTGTTTAACCAGACAGAGTGAGTGCTAAGAGAGCTC    1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GCCCAGGGGTGTCAATCTGGACTGTGTTTAACCAGACAGAGTGAGTGCTAAGAGAGCTC    1080

Qy     1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGGTGAAACTTCCGA    1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGGTGAAACTTCCGA    1140

Qy     1141 GCGACGGCAGCCTTTGAAATGGGCGCGACTGATTGAGGCGCTCCTTCCCTGCTGGACAGC    1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GCGACGGCAGCCTTTGAAATGGGCGCGACTGATTGAGGCGCTCCTTCCCTGCTGGACAGC    1200

Qy     1201 AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGTGACATCCTA    1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGTGACATCCTA    1260

Qy     1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGCACCAGCGTGCGGTTCCTTGTTGTCACGGATGAGA    1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGCACCAGCGTGCGGTTCCTTGTTGTCACGAGATGAGA    1320

Qy     1321 AGGCAGCACAGAAGGGGGGACCAAAGGGAGGGGTGTGAGGCTACCGCCCCAGCACGAGAGGGTAGCCGAG    1380
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Db 1321 AGGCACGACAAGGGAGGGACCAAAGGGGTGTGAGCTACCGCGCACGCAGAGGTAGCCGAG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGGAATGTGGAGAAGCCAGCCAGAGGCATCTGAGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGGAATGTGGAGAAGCCAGCCAGAGGCATCTGAGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1441 GGAGCCGGTAACTGTCCTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 GGAGCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1501 TTTTAAAATAAATATTTATAAT 1522
         ||||||||||||||||||||||
Db 1501 TTTTAAAATAAATATTTATAAT 1522

RESULT 3
AAA52459
ID   AAA52459 standard; cDNA; 1522 BP.
XX
AC   AAA52459;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human MN cDNA.
XX
KW   MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW   proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW   abnormal expression; neoplastic disease; cancer; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            13..1392
FT                  /tag= a
FT                  /product= "Human MN protein"
XX
PN   WO20024913-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;  99WO-US024879.
XX
PR   23-OCT-1998;  98US-00177776.
PR   23-OCT-1998;  98US-00178115.
XX
PA   (FARB ) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J, Pastorekova S, Pastorek J;
XX
DR   WPI; 2000-350752/30.
DR   P-PSDB; AAB03005.
XX
PT   A molecule which specifically binds to a site on MN protein (oncoprotein)
PT   and prevents adhesion of vertebrate cells to the protein, useful for
PT   treating preneoplastic or neoplastic diseases such as cancer.
XX
PS   Example 1; Fig 1A-C; 154pp; English.
XX
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CC The invention relates to the inhibition of cell adhesion mediated by the
CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC protein). The MN protein is a tumour-associated adhesion molecule which
CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC Abnormal expression of the MN protein is associated with tumorigenicity.
CC The invention encompasses molecules (e.g., proteins and peptides) which
CC specifically bind to a site on the MN protein, thereby preventing
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC also encompasses MN proteins or MN protein fragments which can be added
CC to the extracellular environment to prevent the adhesion of vertebrate
CC cells to each other. The invention also relates to the identification of
CC the binding site of the MN protein and to a method of identifying a site

CC on an MN protein to which cells adhere, comprising testing a series of
CC overlapping peptides from the protein in a cell adhesion assay. The
CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domain of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (AAB03035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a nucleic
CC acid encoding a cytotoxic protein or peptide operatively linked to a MN
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC and peptides, and expression vectors encoding such proteins and peptides
CC are useful for treating patients with preneoplastic or neoplastic disease
CC (e.g., cancers) associated with or characterised by abnormal MN
CC expression. The present sequence represents cDNA encoding the human MN
CC protein

```
SQ  Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match    100.0%;  Score 1522;  DB 3;  Length 1522;
Best Local Similarity   100.0%;     Pred. No. 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1 ACAGTCAGCGCAATGGCTCCCCTCCCCTGCCCCCAGCCCTGGCCTCCCTCTGTTGATCCGGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ACAGTCAGCGCAATGGCTCCCCTCCCCTGCCCCCAGCCCTGGCCTCCCTCTGTTGATCCGGCC 60

Qy    61 CCTGCTCCAGGCCTCACTGTCGAAACTGCTGCGTGTCACTGTCCTTTCTCGATGGCCTTCCAT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCTGCTCCAGGCCTCACTGTCGAAACTGCTGCGTGTCACTGTCCTTTCTCGATGGCCTTCCAT 120

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTCTTCTGGGGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTCTTCTGGGGAA 180

Qy   181 GATGACCCACTCGGGCGGAGGAGGATCTGCCCAGTGAAGGAGGGATTCACCCAGAGGAGGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATGACCCACTCGGGCGGAGGAGGATCTGCCCAGTGAAGGAGGGATTCACCCAGAGGAGGAT 240

Qy   241 CCACCCGGAGAGGAGGAGATCTACCTGGAGGAGGAGGAGGATCTACCT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACCCGGAGAGGAGGAGATCTACCTGGAGGAGGAGGAGGATCTACCT 300

Qy   301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Qy   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACCAGGGACACAAAGAAGGGAT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACCAGGGACACAAAGAAGGGAT 420

Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGGGACCCGGCCCTGGCCGTGTCCCCGGGATCCTGC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGAGTCATTGGGCGCTATGGAGGGGACCCGGCCCTGGCCGTGTCCCCGGGATCCTGC 480

Qy   481 GCGGGGCCGCTTCCAGTCCCGGGGATATCCGGCGCCCAGCTCGCCGCCCGGCCTTCCCCGGCC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCGGGGCCGCTTCCAGTCCCGGGGATATCCGGCGCCCAGCTCGCCGCCCGGCCTTCCCCGGCC 540

Qy   541 CTGCGCGCCCCTGGAACTCCTGGGCTTCCACGACTCCCAGAACTGGCCTGGCTGGC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGCGCGCCCCTGGAACTCCTGGGCTTCCACGACTCCCAGAACTGGCCTGGCTGGC 600

Qy   601 AACAATGCCACAGTGTGCAACTGACCCTGCCTAGAGATGGCCTCTGGGTCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACAATGCCACAGTGTGCAACTGACCCTGCCTAGAGATGGCCTCTGGGTCC 660

Qy   661 CGGCGGGAGTACCGGCTCTGCAGCTGCATCTGACCCTGCCTGGTGTCCGGGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CGGCGGGAGTACCGGCTCTGCAGCTGCATCTGACCCTGCCTGGTGTCCGGGC 720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCCGTTCCCTGCGAGATCCACGTGGTTCACCTCAGC 780
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RESULT 4
ID    ADG31413 standard; cDNA; 1522 BP.
XX
AC    ADG31413;
XX
DT    26-FEB-2004  (first entry)
XX
DE    Human MN cDNA SeqID 1.
XX
KW    human; gene; 'ss; monoclonal antibody; MN/CA IX; MN; oncogene;
KW    carbonic anhydrae 9; CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250;
KW    neoplastic tumour; cytostatic; cancer; tumour therapy;
KW    anti-tumour vaccine.
XX
OS    Homo sapiens.
XX
PN    WO200310029-A2.
XX
PD    04-DEC-2003.
XX
PF    22-FEB-2003; 2003WO-US005136.
XX
PR    23-MAY-2002; 2002US-03830068P.
PR    05-DEC-2002; 2002US-0431499P.
XX
PA    (FARB ) BAYER CORP.
PA    (VIRO-) INST VIROLOGY.
XX
PI    Pastorek J,  Pastorekova S,  Zatovicova M,  Zavada J,  Ortova Gut M;
XX
DR    WPI; 2004-035136/03.
DR    P-PSDB; ADG31414.
XX
PS    Disclosure; SEQ ID NO 1; 156pp; English.
XX
CC    This invention relates to a novel monoclonal antibody identified as the
CC    MN/CA IX specific antibody prepared in knockout mice ('CA IX deficient
CC    mice). Specifically, this antibody is directed towards the MN gene, a
CC    cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
CC    MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
CC    isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
CC    present invention describes the generation of this monoclonal antibody,
CC    and immunoreactive fragments thereof, which are directed against non-
CC    immunodominant epitopes on the CA IX extracellular domain. As such, this
CC    antibody can be useful diagnostically as a marker for preneoplastic/
CC    neoplastic tumours. Accordingly, compositions exhibit cytostatic activity and are
CC    approaches. According to the diagnosis, prognosis and treatment of various cancers
CC    useful in the diagnosis, prognosis and treatment of various cancers
CC    including breast, bladder or lung cancer, in tumour therapy and in anti-
CC    tumour vaccination. This polynucleotide sequence is the human MN cDNA of
CC    the invention.
XX
SQ    Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
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Query Match             100.0%;  Score 1522;  DB 12;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;    Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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Qy          1 ACAGTCAGCCGCATGGACTCCCCGTGTGCCCCAGCCCCTGCTCCCTCCGGCC          50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACAGTCAGCCGCATGGACTCCCCGTGTGCCCCAGCCCCTGCTCCCTCCGGCC          60

Qy         61 CCTGCTCCAGGCCTCACTGTGGTCAACTGCTGCTGCTTCTGAGTGCCCATCCAT        120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCTGATGCCGGCCCAT         120

Qy        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGGCTCTTCTCGGGAA        180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGGCTCTTCTCGGGAA        180

Qy        181 GATGACCCACTGGGCGCGAGGAGGGATCTGCCCAGTGAAGAGGAGGATT        240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGACCCACTGGGCGCGAGGAGGGATCTGCCCAGTGAAGAGGAGGATT        240

Qy        241 CCACCCGGACGAGGAGGATCTTACCTGGAGGAGGAGGATCTACCT        300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACCCGGACGAGGAGGATCTTACCTGGAGGAGGAGGATCTACCT        300

Qy        301 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGCTTCCTGAGAGTTAGAGGATCTTACTTGTT        360
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Db        301 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGCTTCCTGAGAGTTAGAGGATCTTACTTGTT        360

Qy        361 GAGGCTTCCTGGAGATCCCAAGAACCCCAGAATAATGCCCACCAGGGACAAAAGAAGGGGAT        420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        721 TCCGAGCACACTGTGGAAGGCCACACCGTTTCCCTGCCAGATCCACGTGGTTCACCTCAGC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCGGCCCTTGCCAGAGTTGACGAGGCCACACCGTTTCCCTGCCAGATCCACGTGGTTGGCC        780

Qy        781 ACCGGCCCTTGCCAGAGTTGACGAGGCCCTTGGGCGCCCGGAGGAGGCCCTGGCCGTTGGCC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCGGCCCTTGCCAGAGTTGACGAGGCCCTTGGGCGCCCGGAGGAGGCCCTGGCCGTTGGCC        840

Qy        841 GCCTTTCTGGAGGAGGGGCCCCGGAAGAAAAACAGTGCCTATGAGGCAGTTGCTGTCTCGCTTG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCCTTTCTGGAGGAGGGGCCCCGGAAGAAAAACAGTGCCTATGAGGCAGTTGCTGTCTCGCTTG        900

Qy        901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC        960

Qy        961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGATGAGGGGTCTCTGACTACACACCCCCTGT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGATGAGGGGTCTCTGACTACACACCCCCTGT       1020

Qy       1021 GCCCAGGGGTGTCATTCTGACTGTGTTTAACCAGACAGAGCTGAGTGAGTGCTAAGCAGCTC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCCAGGGGTGTCATTCTGACTGTGTTTAACCAGACAGAGCTGAGTGAGTGCTAAGCAGCTC       1080

Qy       1081 CACACCCTTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CACACCCTTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA       1140

Qy       1141 GCGACGCAGCCCTTTGAATGGGGCGAGTGATTGAGGGTCTCCTTCCCTGCTCGGAGTGGGACAGC
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCGACGCAGCCCTTTGAATGGGGCGAGTGATTGAGGGTCTCCTTCCCTGCTCGGAGTGGGACAGC       1200

Qy       1201 AGTCCTCCGGGCGTGCTGAGCCAGTGAATTCCTCGGCTGCTTGGTGACATCCTA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTCCTCCGGGCGTGCTGAGCCAGTGAATTCCTCGGCTGCTTGGTGACATCCTA       1260

Qy       1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGGGTCGGTTCCTTGTCAGATGAGA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGGGTCGGTTCCTTGTCAGATGAGA       1320

Qy       1321 AGGCAGGACAGGAGAGGGGAACCAAAAGGGGGGTGTGGAGCTACCGGCCGAG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGGCAGGACAGGAGAGGGGAACCAAAAGGGGGGTGTGGAGCTACCGGCCGAG       1380

Qy       1381 ACTGGGAGCCCTAGAGGCTTGGAGAATGTGAGAAGCCAGCCAGGCATCTGAGG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 ACTGGGAGCCCTAGAGGCTTGGAGAATGTGAGAAGCCAGCCAGGCATCTGAGG       1440

Qy       1441 GGAGCCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GGAGCCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT       1500

Qy       1501 TTTTAAAAATAAATATTTATAAT
              |||||||||||||||||||||||
Db       1501 TTTTAAAAATAAATATTTATAAT       1522
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Db   361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAATAATGTCCCACCAGGGACCAGGACGGGGAT 420

Qy   421 GACCAGAGTCATTGGGCGTCTATGCAGGGCGACCCCGGGTGGTGTCCCCAGCCGTGGCCTGC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGAGTCATTGGGCGTCTATGCAGGGCGACCCCGGGTGGTGTCCCCAGCCGTGGCCTGC 480

Qy   481 GCGGGGCCGCCTTCCAGTCCCGGTGGGCGATATCCGCCCACCAGCTCGGCCGCCTTCTGGCGGCGCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCGGGGCCGCCTTCCAGTCCCGGTGGGCGTATATCCGCCCACCAGCTCGGCCGCCTTCTGGCGGCC 540

Qy   541 CTGGCGCCCCCTGGAAACTCCTGGGCTTTCAGCGCTCCCAGAACTGCCCTGCGGC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGGCGCCCCCTGGAAACTCCTGGGCTTTCAGCGCTCCCAGAACTGCCCTGCGGC 600

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGCGCTGGATATCCGGGCGGGTCCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGCGCTGGATATCCGGGCGGGTCCC 660

Qy   661 GGGCGGGGAGTACCGGGGCTTCGCAGCTGCATCTGCACTGGGGGCTCGCAGGTCGCGGGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGGCGGGGAGTACCGGGGCTGCGAGCTGCATCTCGCACTGGGGGCTCGCAGGTCGCGGGC 720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780

Qy   781 ACCGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGCGGCCTTGGGGCGGGCCGTGTTGGCC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACCGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGCGGCCTTGGGGCGGGCCGTGTTGGCC 840

Qy   841 GCCTTTCTGGAGGACGGCCACCGTTTCCTGCCGGAGTCCACGTGGTTCACCTCAGC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCCTTTCTGGAGGACGGCCACCGTTTCCTGCCGGAGTCCACGTGGTTCACCTCAGC 900

Qy   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACGTGGACATATCTGCACTC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACGTGGACATATCTGCACTC 960

Qy   961 CTGCCCCTTCTGACTTCAGCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGCCTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CTGCCCCTTCTGACTTCAGCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGCCTGT 1020

Qy 1021 GCCCAGGGGTGCATCTGGACTGTGTTTAACCAGACAGTGATCGTGCTGCTTAAGCAGCTC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GCCCAGGGGTGCATCTGGACTGTGTTTAACCAGACAGTGATCGTGCTGCTTAAGCAGCTC 1080

Qy 1081 CACACCCCTCTCTGACACCCGTGGGGACCCTGGGTGACTCTCGGCTCACAGCTCGAACTTCCGA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CACACCCCTCTCTGACACCCGTGGGGACCCTGGGTGACTCTCGGCTCACAGCTGAACTTCCGA 1140

Qy 1141 GCCGAGAGGTGTCATCTGGACTGTGTTTAACCAGACAGTGCTGCTAAGCAGCTC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GCCGAGAGGTGTCATCTGGACTGTGTTTAACCAGACAGTGCTGCTAAGCAGCTC 1200

Qy 1201 AGTCCTCCGGGCTGCTGAGCCAGTCCACTGAATTCCTGGCTGCTCTGGGGTACACATCCTA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AGTCCTCCGGGCTGCTGAGCCAGTCCACTGAATTCCTGGCTGCTCTGGGGTACACATCCTA 1260

Qy 1261 GCCCTCGGTTTTTGGCCTCCTTTTGTCTCACCAGCGGCGTTCCTTGTGTCCAGATGAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GCCCTCGGTTTTTGGCCTCCTTTTGTCTCACCAGCGGCGTTCCTTGTGTCCAGATGAGA 1320

Qy 1321 AGGCAGCAGAGAGGGGGAACCAAAGGGGGTGTGAGCTACCCGCCACCGCCAGGTAGCCGAG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 AGGCAGCAGAGAGGGGGAACCAAAGGGGGTGTGAGCTACCCGCCACCGCCAGGTAGCCGAG 1380

Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCATCTGAGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCATCTGAGGG 1440

Qy 1441 GGAGCCGGTAACTGTTCTGTCGTGCTCATTAATGCCACTTCTTCTTTTTAACTGCCAAGAAATT 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 GGAGCCGGTAACTGTTCTGTCGTGCTCATTAATGCCACTTCTTCTTTTTAACTGCCAAGAAATT 1500

Qy 1501 TTTTAAAAATAAAATATTTTATAAT 1522
         |||||||||||||||||||||||||
Db 1501 TTTTAAAAATAAAATATTTTATAAT 1522

Query Match   100.0%;   Score 1522;   DB 12;   Length 1522;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative 0; Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCTGGCTCCCCTGTTGAATCCGGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCTGGCTCCCCTGTTGAATCCGGCC 60

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Qy    61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTGCTCACTGTTCTCGATGCCTGTGTCCAT 120
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Db    61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGTGTCACTG...                   120

Qy   121 CCCCAGGAGGTTGGCCCCGGATGCAGGAGGAGGAGGATTCCCCCTTGGGGAGGAGGAGGAA 180
         |||||||||||||||||||||
Db   121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGAGGAGGATT...                    180

Qy   181 GATGACCCACTGGGGCAGGAGATCTGCCCAGTGAAGAGGAGGAGGAT              240
Db   181 GATGACCCACTGGGGCGAGGAGATTCGCCCAGTGAAGAGGAGGAT               240

Qy   241 CCACCCCGGAGGAGGGATCTACCTGGAGGAGGAGGATCTACCT                 300
Db   241 CCACCCGGAGGAGGGATCTACCTGGAGGAGGAGGATCTACCT                  300

Qy   301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGCTCCCGGAGGAGGAGGAGG           360
Db   301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGCTCCCGGAGGAGGAGGAGG          360

Qy   361 GAGGCTTCCTGGAGGAGGATCCTCAAGAACCCCCAGAATAAATGCCCACCAGGGGA     420
Db   361 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAATAAATGCCCACCAGGGGAT        420

Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGGGGAGGACCCGGCCCCAGCCTGC           480
Db   421 GACCAGAGTCATTGGGCGCTATGGAGGGGGAGGACCCGGCGCCCCAGCCTGC         480

Qy   481 GCGGGGCCGCCTTCCAGTGCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTCTCCC  540
Db   481 GCGGGCCGCCTTCCAGTGCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTCGCCGCC 540

Qy   541 CTGCGCCCCCCCTGGAACTCCTGGCCTTCCCAGCCTCCCAGCTCCCAGAACTGCGCCTGCGC 600
Db   541 CTGCGCGCCCCTGAACTCCTGGGCTTCCCAGCTCCCAGCTCCCAGAACTGCGCCTGCGC  600

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTGCCTCTGGGCTGAAGATGGCTCTGGGGTCC 660
Db   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCTGGGCTAGAGATGGCTCTGGGTCC   660

Qy   661 GGGCGGGAGTACCGGGCTCTGCAGCTCGCATCTGGGCGGGGGGCTGCAGGTCGTCCGGGC 720
Db   661 GGGCGGGAGTACCGGGGCTCTGCGAGCTCGCATCTGGGCGGGGGGCTGCAGGTCGTCCGGGC 720

Qy   721 TCGGAGCACACTGTGGAAGGGCCACACCGTTTCCCTGCCGAGTCCACGTGGTTCACCTCAGC 780
Db   721 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCGAGTCCACGTGGTTCACCTCAGC  780

Qy   781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCGCGGGGGAGGCCTGGCCCGTGTTGGCC 840
Db   781 ACCGGCCTTGCCAGAGTTGACGAGGCCTTGGGGGCGCGGGGGAGGCCTGGCCCGTGTTGGCC  840

Qy   841 GCCTTTCTGGAGGAGGGGCCCGGGAGAGAAAAACAGTGGCCTATGAGCGAGTTGCTCGTGTGTTGTCTCGCTTG 900
Db   841 GCCTTGGGAGGGGGGCCCGGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCGCTTG   900

Qy   901 GAAGAAAATCGCTGAGGAAGGCTCAGGACTCAGGTCCCAGGACTGGGGACCATATCTGCACTC 960
Db   901 GAAGAAAATCGCTGAGGAAGGCTCAGGACTCAGGTCCCAGGACTGGGGACCATATCTGCACTC 960

Qy   961 CTGCCCTCTGACTTCAGCGCGGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020
Db   961 CTGCCCTCTGACTTCAGCGCGGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020

Qy  1021 GCCCAGGGGTGTCATTCTGGACTGTGTTTTAAACCAGACAGTGATAGTGCTAAGCAGCTC 1080
Db  1021 GCCCAGGGGTGTCATTCTGGACTGTGTTTTAAACCAGACAGTGATAGTGCTAAGCAGCTC 1080

Qy  1081 CACACCCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGGTTGACTCTCAGACTGAACTTCCGA 1140
Db  1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140

Qy  1141 GCGACGCACGCCTTTGAAATGGGGGAGTGATTGAGGGCCTCTTCCCTTGCTGAGTGACAGC 1200
Db  1141 GCGACGCAGCAGCCTTTGAATGGGCGCAGAGTTGAGGGCCTCTTCCCTGCTGAGTGACAGC 1200

Qy  1201 AGTCCCTCGGCGGCTGCTCTGAGCCCAGTCCAGCTGAATTCCTGGCTGGCTGGCTGACATCCTA 1260
Db  1201 AGTCCTCGGCGGCTGCTCAGCCAGTCCAGCTGAATTCCTGCCTGGCTGGCTGACATCCTA 1260

Qy  1261 GCCCTGTGGTTTTGGGGCCTCCCTTTTTGCTGTGCACCAGCGTCGCGGTTCCTTGTGTGCAGATGAGA 1320
Db  1261 GCCCTGTGGTTTTGGGGCCTCCCTTTTTGCTGTGCACCAGCGTCGCGGTTCCTTGTGTGCAGATGAGA 1320

Qy  1321 AGGGCAGCACAGAAGGGGGGAACCAAAGGGGGGTGTGAGCTACCGGTACCGCGAG 1380
Db  1321 AGGGCAGCACAGAGAGGGGGACCAAAGGGGTGTGAGCTACCGGTAGCCGAG   1380

Qy  1381 ACTGGAGCCCTAGAGGCTGGATCTTGGAGGAAGTGTGAGAAGGCCAGCCGGCATCTGAGGG 1440
Db  1381 ACTGGAGCCCTAGAGGCTGGATCTTGGAGGAAGTGTGAGAAGGCCAGCCGGCATCTGAGGG 1440

Qy  1441 GGAGGCCGGTAACTGTCCCTGCTCATTATGCCACTTCCTTTTAAACTGCCCAAGAAATT 1500
Db  1441 GGAGGCCGGTAACTGTCCCTGCTCATTATGCCACTTCCTTTTAAACTGCCCAAGAAATT 1500

Qy  1501 TTTTAAAATAAATATTTTATTAT 1522
Db  1501 TTTTAAAATAAATATTTTATTAT 1522
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RESULT 6
ABL64779
ID   ABL64779 standard; DNA; 1552 BP.
XX
AC   ABL64779;
XX
DT   15-MAY-2002 (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:3116.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235134P.
PR   26-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.

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PR   28-SEP-2000;  2000US-0236028P.
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PR   28-SEP-2000;  2000US-0236034P.
PR   28-SEP-2000;  2000US-0236109P.
PR   28-SEP-2000;  2000US-0236111P.
PR   29-SEP-2000;  2000US-0236842P.
PR   29-SEP-2000;  2000US-0236891P.
PR   02-OCT-2000;  2000US-0237172P.
PR   02-OCT-2000;  2000US-0237173P.
PR   02-OCT-2000;  2000US-0237278P.
PR   02-OCT-2000;  2000US-0237294P.
PR   02-OCT-2000;  2000US-0237295P.
PR   02-OCT-2000;  2000US-0237316P.
PR   02-OCT-2000;  2000US-0237425P.
PR   03-OCT-2000;  2000US-0237598P.
PR   03-OCT-2000;  2000US-0237604P.
PR   03-OCT-2000;  2000US-0237606P.
PR   03-OCT-2000;  2000US-0237608P.
PR   01-NOV-2000;  2000US-0244867P.
PR   01-NOV-2000;  2000US-0245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PB, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Claim 1; SEQ ID NO 3116; 44pp; English.
PS   Claim 1; SEQ ID NO 3116; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

     Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
     Best Local Similarity   100.0%;
     Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 ACAGTCAGCCGCCATGGCTCCCCTGTCGCCCAGCCTCCCTCGTTGATCCCCGCC 60
Db        31 ACAGTCAGCCGCCATGGCTCCCCTGTCGCCCAGCCTCCCTCGTTGATCCCCGCC 90

Qy        61 CCTGCTCCAGGCCCTCACTGTGCACTGCTGCTTCTTCGATGCCTGTTCCAT 120
Db        91 CCTGCTCCAGGCCCTCACTGTGCACTGCTGCTTCTTCGATGCCTGTTCCAT 150

Qy       121 CCCCAGGAGGTTGCCCCGGGCGATGCAGGAGGATTCCCCGCTCTTCTGGGGAA 180
Db       151 CCCCAGAGGTTGCCCCGGGCGATGCAGGAGGATTCCCCGCTCTTCTGGGGAA 210

Qy       181 GATGACCCACTGGGCGAGGAGATCTGCCCAGTGAGAGGAGGAGGAGGATGAGA 240

Db       211 GATGACCCACTGGGCGCGAGGAGGAGGAGGATTCACCCGAGAGGAGGAT 270
Qy       241 CCACCCGAGAGGAGGAGGAGGATCTACCTGGGAGGAGGAGGAGGATCTACCT 300
Db       271 CCACCCGAGAGGAGGAGGATCTACCTGGGAGGAGGAGGAGGATCTACCT 330

Qy       301 GAAGTTAAGCCTAAATCAGGAGGAGGAGGGGCTCCCTGAAGTTAGAGGATCTACTGTT 360
Db       331 GAAGTTAAGCCTAAATCAGGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACTGTT 390

Qy       361 GAGGCTCCTGGGAGATCTCAAGAACCCCAGAAATAAATGCCCACAGGGACAAAGAGGGGAT 420
Db       391 GAGGCTCCTGGGAGATCTCAAGAACCCCAGAAATAAATGCCCACAGGGACAAAGAGGGGAT 450

Qy       421 GACCAAGGAGTCATTGGGCGCTATGAGGGGACACCCCGGCCCTTGCC 480
Db       451 GACCAGAGTCATTGGGCGCTATGAGGGGACACCCCGGCCCTTGCC 510

Qy       481 GCGGGCCCGCTTCCAGTCCCCGGTGGATATCCCGCCCCCCAGCTCGGCCCGGCC 540
Db       511 GCGGGCCCGCTTCCAGTCCCCGGTGGATATCCCGCCCCCCAGCTCGGCCCGGC 570

Qy       541 CTGCGCCCCCTGAAACTCCTGGGCTTCCAGCCTCCCAGAACTGCCCTGCGC 600
Db       571 CTGCGCCCCTGGAAACTCCTGGGCTTCCAGCCTCCCAGAACTGCCCTGCGC 630

Qy       601 AACAATGCCACAGTGTGCAACTGACCCTGCCTTCAGCTCCCGGCTAGAGATGGCTCC 660
Db       631 AACAATGCCACAGTGTGCAACTGACCCTGCCTTCAGCTCCCGGCTAGAGATGGCTCC 690

Qy       661 GGGCGGGGAGTACGGGGCTCTCAGCGCTGCAGCTGCAGGTGCTGCAGGTCGTCCGGC 720
Db       691 GGGCGGGGAGTACCGGGGCTCTCGACGCTGCAGCTGCAGGTGCTGCAGGTCGTCCGGC 750

Qy       721 TCGGAGCACACGTGGAAGGGCCACCGTTTCCCTGCCGAGATCCACGTCGTTCACCTCAGC 780
Db       751 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCGAGATCCACGTCGTTCACCTCAGC 810

Qy       781 ACCGGCCTTTGCCAGAGTTGACCGAGGCCACCGTTTCCCGGAGATCCACGTCGTTGGCC 840
Db       811 ACCGGCCTTTGCCAGAGTTGACCAGGCCCTTGGGGTCGGGGGAGGCCTGGCCGTGTTGGCC 870

Qy       841 GCCTTTCTTGGAGGAGGGCCGGAGAGAAACAGTGTCCTATGAGCAGTTGCTCGTCGCTTG 900
Db       871 GCCTTTCTTGGAGGAGGGCCCCGAGAGAAACAGTGCCTATGAGCAGTTGCTCGTCGCTTG 930

Qy       901 GAAGGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGAAGCATATCTGCACTC 960
Db       931 GAAGGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGAAGCATATCTGCACTC 990

Qy       961 CTGCCCCCTGACTTCAGCCGCTTCTCCAAATATGAGGGGGTCTCTGACTACCACGCCCCGT 1020
Db       991 CTGCCCCCTGACTTCAGCCGCTTCTCCAAATATGAGGGGGTCTCTGACTACCACGCCCCGT 1050

Qy      1021 GCCCCAGGGGTGTCATCTGGACTGTTTAACCAGACACTGAATGCTGAGTGCTAAGCAGCTC 1080
Db      1051 GCCCAGGGGTGTCATCTGGACTGTTTAACCAGACACTGAATGCTGAGTGCTAAGCAGCTC 1110

Qy      1081 CACACCCTTCTGACACCCTGTGGGGGACCTGGTGACTCTGGGGTACAGCTGAACTTCCGA 1140
Db      1111 CACACCCTTCTCTGACACCCTGTGGGGGACCTGGTGACTCTGGGGTACAGCTGAACTTCCGA 1170

Qy      1141 GCGACGCAGCCTTTGAATGGGCGACCTGGTGGGGACGTGGGACTTCGGGGGTGGAGTGGACAGC 1200
Db      1171 GCGACGCAGCCTTTGAATGGGCGACCTGGTGAGTGGGGACGTGGGACTTCGGGGGGTGGAGTGGACAGC 1230

Qy      1201 AGTCCCTCGGGTGCTGCAGCCAGTCCAGCTGAATTCCTTCGCTGCCTGAATTCCTGCTGCAGCATCCTA 1260
Db      1231 AGTCCCTCGGGCGTCTGAGCCAGTCGAATTCCTGCCTGCTGCCTGAATTCCTGCTGCAGCATCCTA 1290

Qy      1261 CCCCAGAGGTTGCCCCCGGATGCAGGAGGAATTCCCCGGTTCCTTGTTGCAGATGAGA 1320
Db      1291 GCCCTGGTTTTTGGGCGTCCCTTTTTGCTGTGTCACCAGCGTCGCGGTTCCTTGTTGCAGATGAGA 1350
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Qy  1321 AGGCAGCAGCAGGAGGGGAACCAAAGGGGGGGTGTGAGCTACCGGCCGCCCAGCAGCAGAGAGGGTAGCCGAG 1380
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Db  1351 AGGCAGCAGCAGGAGGGGAACCAAAGGGGGGGTGTGAGCTACCGGCCGCCCAGCAGCAGAGAGGGTAGCCGAG 1410

Qy  1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGGAATGTGGAGAAGCCAGCCAGAGGCCATCTGAGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGGAATGTGGAGAAGCCAGCCAGAGGCCATCTGAGGG 1470

Qy  1441 GGAGCCGGTAACTGTCCTGTGCTCCTTCCTTTTAACTGCCAAGAAATT 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1471 GGAGCCGGTAACTGTCCTGTGCTCCTTCCTTTTAACTGCCAAGAAATT 1530

Qy  1501 TTTTAAAATAAAATATTTATAAT 1522
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Db  1531 TTTTAAAATAAAATATTTATAAT 1552
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RESULT 7
ABL62179

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ID   ABL62179 standard; DNA; 1552 BP.
XX
AC   ABL62179;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Colon adenocarcinoma related gene sequence SEQ ID NO:516.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   20-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   22-SEP-2000; 2000US-0234923P.
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PR   25-SEP-2000; 2000US-0235131P.
PR   25-SEP-2000; 2000US-0235280P.
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PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
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PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0271722P.
PR   02-OCT-2000; 2000US-0271737P.
PR   02-OCT-2000; 2000US-0372278P.
PR   02-OCT-2000; 2000US-0372294P.
PR   02-OCT-2000; 2000US-0372295P.
PR   02-OCT-2000; 2000US-0373316P.
PR   03-OCT-2000; 2000US-0374425P.
PR   03-OCT-2000; 2000US-0375598P.
PR   03-OCT-2000; 2000US-0376604P.
PR   03-OCT-2000; 2000US-0376606P.
PR   01-NOV-2000; 2000US-0376608P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene or of a signature gene set.
XX
PS   Claim 1; SEQ ID NO 516; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (1) of a signature gene set, where (1)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL1664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (1) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
```

```
Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 ACAGTTCAGCCGCCATGGCTCTCCCCTGTGCCCCAGCCCCTGTCCCCTCTTGTTGATTCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTTCAGCCGCCATGGCTCTCCCCTGTGCCCCAGCCCCTGTCCCCTCTTGTTGATTCCCGGCC 90

Qy     61 CCTGGTCCAGGCCCTCACTGTGCAACTGCGTGCTGCTCCTTCTGATGCCTGTCCAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGGTCCAGGCCCTCACTGTGCAACTGCGTGCTGCTCCTTCTGATGCCTGTCCAT 150

Qy    121 CCCCAGAGGTTGCCCGGGATCGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGAA 180
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    151 CCCCAGAGGTTGCCCGGGATGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGAA 210

Qy    181 GATGACCCACTGGGCGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 270

Qy    241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAGAGGGGAT 420
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Db   391 GAGGCCTTCCTGGAGATCCTCAAGAACCCCAGAGAATAATGCCCACAGGACAAAAGAAAGGGGAT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 GACCAGAGTCATTGGCGCTATGGAGGCGGACACCGGGCCTTGGCCGGGGTGTCCCCAGCCTTGC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 GACCAGAGTCATTGGCGCTATGGAGGCGGACACCGGGCCTTGGCCGGGGTGTCCCCAGCCTTGC 510

Qy   481 GCGGGGCCGGCTTCCAGTCCCCGGGTGGGATATCCGGCCCGCCGCGCCGCTTCTGCCCGGCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCGGGGCCGGCTTCCAGTCCCCGGGTGGGATATCCGGCCCGCCGCGCCGCTTCTGCCCGGCC 570

Qy   541 CTCGCGCCCCTGGGCGCTTCAGCTCCTGGGGTGGGGCCGGGGTGGGCGCGCCGCCTGGGC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 CTCGGCACCCCTGGGAACTCCTGGGGCTTCAGCTCCTGGGGTGGGGCCGGGGTGGGCGCGCCGCCTGGGC 630

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGGCTTCTCTGGGCTAGAGATGGCTCTGGGGTCCC 660
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Db   631 AACAATGGCCACAGTGTGCAACTGACCCTGGCTTCTCTGGGCTAGAGATGGCTCTGGGGTCCC 690

Qy   661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTCCGGGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTCCGGGC 750

Qy   721 TCCGAGCACACACTGTGGAAGGGCCACACCGTTTCCCGGGAGATCCACGTGGTTCACCTCAGC 780
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Db   751 TCCGAGCACACACTGTGGAAGGGCCACACCGTTTCCCGGGAGATCCACGTGGTTCACCTCAGC 810

Qy   781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCGCCGCCGGGGAGGGCCTTGGCCGGTGTTGGCC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCGCCGCCGGGGAGGGCCTTGGCCGGTGTTGGCC 870

Qy   841 GCCTTTCTGGAGGAGGGCCCGGAGAAAACAGTGCCTATGAGTTGTGTCTCGCTTG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 GCCTTTCTGGAGGAGGGCCCGGAGAAAACAGTGCCTATGAGTTGTGTCTCGCTTG 930

Qy   901 GAAGAAATCGCTGAGGAAGGGCTCAGGGACTCAGGTCCAGGACTGGACATATCTGCACTC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 GAAGAAATCGCTGAGGAAGGGCTCAGGGACTCAGGTCCAGGACTGGACATATCTGCACTC 990

Qy   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGCCCTCTGACTTCAGCGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGT 1050

Qy  1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAGTGCTAAGCAGCTC 1080
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Db  1051 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAGTGCTAAGCAGCTC 1110

Qy  1081 CACACCCCTCTCGACACCCTGTGGGACCTGGTGACTCTGGCTACAGCTTCCGA 1140
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Db  1111 CACACCCCTCTCGACACCCTGTGGGACCTGGTGACTCTGGCTACAGCTTCCGA 1170

Qy  1141 GCCCAGCGAGCCCTTTGAATGGGGCCTTCCTGGAGTGGGGACAGC 1200
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Db  1171 GCCCAGCGAGCCCTTTGAATGGGGCCTTCCTGGAGTGGGGACAGC 1230

Qy  1201 AGTCCTTCGGGCTTCGAGCCAGTCCAGCTGGAATTCCTGGCCTGGCTGCTGCTGGTGGTTGGACATCCTA 1260
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Db  1231 AGTCCTTCGGGCTTCGAGCCAGTCCAGCTGGAATTCCTGGCCTGGCTGCTGCTGGTGGTTGGACATCCTA 1290

Qy  1261 GCCCTGGTTTTTGGCCTCCTTTTTGTCTCAGCAGGTGCGCGCGTTCCTTGGTCAGAGATGAGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1291 GCCCTGGTTTTTGGCCTCCTTTTTGTCTCAGCAGGTGCGCGCGTTCCTTGGTCAGAGATGAGA 1350

Qy  1321 AGGCAGCACAGAAAGGGGAAACCAAAAGGGGTGTGAGCTACCGGCTACGAGTAGCCGAG 1380
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Db  1351 AGGCAGCACAGAAAGGGGAAACCAAAAGGGGTGTGAGCTACCGGCTACGAGTAGCCGAG 1410

Qy  1381 ACTGGGAGCCCTAGAGGCTGGGATCTTGGAGAAGTGAGAAGCCAGCCGAGGCATCTGAGGG 1440
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Db  1411 ACTGGGAGCCCTAGAGGCTGGGATCTTGGAGAAGTGAGAAGCCAGCCGAGGCATCTGAGGG 1470

Qy  1441 GGAGCCGGGTAACTGTCCTGTCCCTGCTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAAATT 1500
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Db  1471 GGAGCCGGGTAACTGTCCTGTCCCTGCTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAAATT 1530

Qy  1501 TTTTAAAATAAAATATTTATTAAT 1522
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Db  1531 TTTTAAAATAAAATATTTATTAAT 1552
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RESULT 8
ABL65416
ID   ABL65416 standard; DNA; 1552 BP.
XX
AC   ABL65416;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:3753.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0231313P.
PR   18-SEP-2000; 2000US-0231133P.
PR   20-SEP-2000; 2000US-0236117P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   20-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   26-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   27-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   02-OCT-2000; 2000US-0237316P.
PR   03-OCT-2000; 2000US-0237425P.
PR   03-OCT-2000; 2000US-0237598P.
PR   03-OCT-2000; 2000US-0237604P.
PR   03-OCT-2000; 2000US-0237606P.
PR   03-OCT-2000; 2000US-0237608P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX
```

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PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene of a signature gene set.
XX
PS   Claim 1; SEQ ID NO 3753; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL1664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. M1 has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
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Best Local Similarity    100.0%;
Matches 1522;  Conservative  0;   Mismatches  0;  Indels  0;  Gaps  0;

Qy           1 ACAGTCAGCCGCATGGCGTTCCCGGCTCCCTGTGCCCCGGCTCCCCAGCCCTCGTTGATCCCGGCC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ACAGTCAGCCGCATGGCGTTCCCGGCTCCCTGTGCCCCGGCTCCCCAGCCCTCGTTGATCCCGGCC 60
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AC   ABL68346;
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DT   15-MAY-2002  (first entry)
XX
DE   Kidney cancer related gene sequence SEQ ID NO:6683.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2OO194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   02-OCT-2000; 2000US-0237316P.
PR   03-OCT-2000; 2000US-0237425P.
PR   03-OCT-2000; 2000US-0237598P.
PR   03-OCT-2000; 2000US-0237604P.
PR   03-OCT-2000; 2000US-0237606P.
PR   03-OCT-2000; 2000US-0237608P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene of a signature gene set.
XX
PS   Claim 1; SEQ ID NO 6683; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1522;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 ACAGTCAGCGCGCATGGCTCTCCCCCTGTTGCCCCAGCCCCTCCCTCCTTCTGTTGATCCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ACAGTCAGCGCGCATGGCTCTCCCCCTGTTGCCCCAGCCCCTCCCTCCTTCTGTTGATCCCGGCC 90

Qy         61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCGTTCTGATGCCTTGTCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCGTTCTGATGCCTTGTCCAT 150

Qy        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCCTTGGGAGGAGGCTCTTTCTGGGGAA 180
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Db        151 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCCTTGGGAGGAGGCTCTTTCTGGGGAA 210

Qy        181 GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAAGGAATTCACCCAGAGAGGAGGAT 240
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Db        211 GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAAGGAATTCACCCAGAGAGGAGGAT 270

Qy        241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy        301 GGAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GGAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy        361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAAGAAGGGGAT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAAGAAGGGGAT 450

Qy        421 GACCAGAGTCATTGGGCGCTATGGAGGGCGACACCGGCGCCTGGGCCCCGGGGTGTCCCCGCTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GACCAGAGTCATTGGGCGCTATGGAGGGCGACACCGGCGCCTGGGCCCCGGGGTGTCCCCGCTGC 510

Qy        481 GCGGGCGCGCTTCCAGTCCCCGGTGGATATCCGGCCGCCGCCGCCTTCTCCGGCC 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GCGGGCGCGCTTCCAGTCCCCGGTGGATATCCGGCCGCCGCCGCCTTCTCCGGCC 570

Qy        541 CTCGCGCCCCCTCGAACTCCTCGGCTTCCAGCTCCCGCGCCCTGCGCCCTGCGC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTGCGCGCCCCCTGGAACTCCTCGGCTTCCAGCTCCCGCGCCCTGCGCCCTGCGG 630

Qy        601 AACAATGGCCCACAGTGTGCAACTGACCCTGCCTCTTCCTGCGGCCTAGAGATGGCTCTGGGGTCCC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 AACAATGGCCCACAGTGTGCAACTGACCCTGCCTCTTCCTGCGGCCTAGAGATGGCTCTGGGGTCC 690

Qy        661 GGGCGGGAGGTACCGGGGCGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTCCGGCGC 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GGGCGGGAGGTACCGGGGCGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTCCGGGC 750
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Qy    721 TCGGAGCACACTGTGGGAAGGGCCACCGGTTTCCCTGCCCGAGATCCACGTGGTTCACCTCAGC 780
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Db    751 TCGGAGCACACTGTGGGAAGGGCCACCGGTTTCCCTGCCCGAGATCCACGTGGTTCACCTCAGC 810

Qy    781 ACCGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGGCCCGGGAGGCCTGGCCCGTGGGCGTGTTGGCC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ACCGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGGCCCGGGAGGCCTGGCCCGTGGGCGTGTTGGCC 870

Qy    841 GCCTTTCTGGAGGAGGGCCGGGAAGAAAACAGTGCCCTATGAGCAGTTGCTTGTCTCGCTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTCTGGAGGAGGGCCCCGGAGAAAAACAGTGCCCTATGAGCAGTTGCTTGTCTCGCTTG 930

Qy    901 GAAGAAAATCGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGACACATATCTGCACTC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 GAAGAAAATCGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGACACATATCTGCACTC 990

Qy    961 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1050

Qy   1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCCAGCTC 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCCAGCTC 1110

Qy   1081 CACACCCTTCTCTGACACCGGTGGGGGACCTGGTTGACTGAATTCCTGGCTGGTGACATCCTA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 CACACCCTTCTCTGACACCCTGTGGGGACTCGGTTGACTCTCGGCTTGCTGGTGACATCCTA 1170

Qy   1141 GCGACGCAGCAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 GCGACGCAGCAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGGACAGC 1230

Qy   1201 AGTCCCTCGGGGCTGCTGACCCAGTGAATTCCTGCCTGGTGCTGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 AGTCCCTCGGGGCTGCTGACCCAGTGAATTCCTGCCTGGTGCTGGTGACATCCTA 1290

Qy   1261 GCCCTGGTTTTGGCCTCTCCTTTTTGGCGTTCCTTGTGTCAGATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||
Db   1291 GCCCTGGTTTTGGCCTCTCCTTTTTGGCGTTCCTTGTGTCAGATGAGA 1350

Qy   1321 AGGCAGCACGAGAGGGGAACCAAAGGGGGTGTGAGCTACCAGAGGTAGCCGAG 1380
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AGGCAGCACGAGAGGGGAACCAAAGGGGGTGTGAGCTACCAGAGGTAGCCGAG 1410

Qy   1381 ACTGGAGGCCTAGAGGCTGGATCTTGGAGAAGCCGCCCAGAGGCCATCTGAGGG 1440
          |||||||||||||||||||||||||||||||||||||||||||
Db   1411 ACTGGAGGCCTAGAGGCTGGATCTTGGAGAAGCCGCCCAGAGGCCATCTGAGGG 1470

Qy   1441 GGAGCCGCGGTAACTGTCTCCTGCTCATTATGGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GGAGCCGCGGTAACTGTCTCCTGCTCATTATGGCCACTTCCTTTTTAACTGCCAAGAAATT 1530

Qy   1501 TTTTAAAATAAATATTTATAAT 1522
          ||||||||||||||||||||||
Db   1531 TTTTAAAATAAATATTTATAAT 1552
```

Query Match   100.0%; Score 1522; DB 8; Length 1552;
Best Local Similarity   100.0%;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGCCTCCTGTTGATCCCGGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    31 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGCCTCCTGTTGATCCCGGCC 90

Qy    61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTTCTGTGATGCCTGTCCAT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTTCTGTGATGCCTGTCCAT 150

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCCTCTTCTGGGGA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCCTCTTCTGGGGA 210

Qy   181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGAGAGGAT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGAGAGGAT 270

Qy   241 CCACCCGGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
```

```
Db   271 CCACCCCGGGAGAGGAGGATCTACCTGGAGGAGGATCTACCT
         ||||||||||||||||||||||||||||||||||||||||||
Db  1351 AGGCAGCACAGGAAGGGGAACCAAAAGGGGGGTGTGAGCTACCGGCCCAGCAGCAGAGGGTAGCCGAG 1410

Qy   301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGCTCCCTGAAGTTAGGAGAATCTACCTACTGTT 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381 ACTGGAGCCTAGAGGGCTGGGATCTTGGAGAATGTGAGAAGCCAGGCAGCCAGGCAGCCAGGCCATCTGAGG 1440

Db   331 GAAGTTAAGCCTAAATCAGAAGAAGAAGGCTCCCTGAAGTTAGGAGGATCTACCTGTT 390
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGGCCATCTGAGGG 1470

Qy   361 GAGGCTTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACAGGGACAAAGGAAGGGGAT 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441 GGAGGCGGTAACTGTCCTGTCTGCTCATTATGCCACTTCCTTTTAACTGCCCAGAAATT 1500

Db   391 GAGGCTTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACAGGGACAAAGGAAGGGGAT 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1471 GGAGCGGTAACTGTCCGTCCGTCATTATGCCACTTCCTTTTAACTGCCCAGAAATT 1530

Qy   421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCCCTTGCCCCCCAGCCTGC 480
         ||||||||||||||||||||||||||||||||||||||||||||
Qy  1501 TTTTAAAATAAATATATTTATAAT 1522

Db   451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCCCTTGCCCCCCAGCCTGC 510
         ||||||||||||||||||||||||||||||||||||||||||||
Db  1531 TTTTAAAATAAAATATTTATAAT 1552

Qy   481 GCGGGGGCGCTTCCAGTCCCCGGGTGGGATATCCGCGGGGCCCTTCTGCCCGCC 540
Db   511 GCGGGGGCCGCTTCCAGTCCCCGGGTGGGATATCCGCGGCCCTTCTGCCCGCC 570

Qy   541 CTGGCCCCCCCTGGAACTCCTGGGGCTTCAGCTCCCGGCTCCCAGGAACTGCCCCTGCCC 600
Db   571 CTCGGCCCCCCCTGGAACTCCTGGGGCTTCAGCTCCCGGCTCCCAGGAACTGCGCCCTGCCC 630

Qy   601 AACAATGGCCACAGTGTGCAACTGCACCCTGCCCTTCCTGGGCTAGAGATGGCTCTGGGGTCCC 660
Db   631 AACAATGGCCACAGTGTGCAACTGCACCCTGCCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC 690

Qy   661 GGGCGGGGAGTACCGGGCTTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCGTCCCGGGC 720
Db   691 GGGCGGGGAGTACCCGGGCTCTGCACTGGGGGGCTGCAGGTCGTCGTCCCGGGC 750

Qy   721 TCGGGAGCACACTGTGGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGGTTCACCTCAGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 TCGGGAGCACACTGTGGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGGTTCACCTCAGC 810

Qy   781 ACCGCCCTTTGCCCAGAGTTGACGAGGCCTTGGGGCGGAGGCCTGGCCGTTGGCCCGTTTGGCC 840
Db   811 ACCGCCCTTTGCCCAGAGTTGACGAGGGCGCCCGGGAGCCCTGGCCGTTGGCCCGTTTGGCC 870

Qy   841 GCCTTTCTGGGAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGTGAGTGCTAAGCAGCTC 900
Db   871 GCCTTTCTGGGAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGTGAGTGCTAAGCAGCTC 930

Qy   901 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCAGGACTGAGCATATCTGCACTC 960
Db   931 GAAGAAATCGCTGAGGAGGCTCAGAGACTCAGGTCCAGGACTGAGCATATCTGCACTC 990

Qy   961 CTGCCCCTGACTTCAGCCGTACACTTCCAATATGAGGGGGTCTCTGACTACACGCCCTGT 1020
Db   991 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050

Qy  1021 GCCCAGGGGTGTCATCTGGACTCTGTTTAACCAGACACTGACTGACTGCTAAGCAGCTC 1080
Db  1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACACTGACTGACTGACTAAGCAGCTC 1110

Qy  1081 CACACCCCTCTCTGACACACCCGTGGGGACCTGGTCTGGTCTGACTTGGACATTGAACTTCCGA 1140
Db  1111 CACACCCCTCTCTGACACACCCGTGGGGACCTGGTCTGGTCTACAGCTGAACTTCCGA 1170

Qy  1141 GCGACGCGAGCCAGCCCTTTGAATGGGCGAGTGATTGAGGCGACAGC 1200
Db  1171 GCGGACGCGAGCCAGCCCTTTGAATGGGCGGAGTGATTGAGGCGACAGC 1230

Qy  1201 AGTCCTCGGGCGTGCTGAGCCAGTCCACTGCCTGGCGTGCGGTGACATCCCTA 1260
Db  1231 AGTGCCTCGGGCTGCTGAGCCAGTCCACTGCCTGGCGTGCGGTGACATCCTA 1290

Qy  1261 GCCCTGGTTTTTGGGCCTCCCTTTTTGCTGTCACCAGGCTGCCCGTTGCGAGATGAGA 1320
Db  1291 GCCCTGGTTTTTGGGCCTCCCTTTTTGCTGTCACCAGGCGTCCGTTGCGAGATGAGA 1350

Qy  1321 AGGCAGCACAGAGGGGGAACCAAAAGGGGGTGTGAGCTACCGGCCCAGCAGCAGAGGGTAGCCGAG 1380
Db  1351 AGGCAGCACAGAGGGGGAACCAAAAGGGGGTGTGAGCTACCGGCCCAGCAGCAGAGGGTAGCCGAG 1380
```

RESULT 11
ABX76124

XX
ID　ABX76124 standard; DNA; 1552 BP.
XX
AC　ABX76124;
XX
DT　02-APR-2003　(first entry)
XX
DE　Lung cancer-associated polynucleotide #1.
XX
KW　Lung cancer-associated polynucleotide; gene; dg; cytostatic; emphysema;
KW　antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW　small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW　chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW　interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS　Unidentified.
XX
PN　WO20028443-A2.
XX
PD　31-OCT-2002.
XX
PF　18-APR-2002; 2002WO-US012476.
XX
PR　18-APR-2001; 2001US-0284770P.
PR　10-MAY-2001; 2001US-0290492P.
PR　09-NOV-2001; 2001US-0339245P.
PR　13-NOV-2001; 2001US-0350666P.
PR　29-NOV-2001; 2001US-0334370P.
PR　12-APR-2002; 2002US-0372246P.
XX
PA　(EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI　Aziz N,　Murray R;
XX
DR　WPI; 2003-0931611/08.
DR　P-PSDB; ABU56408.
XX
PT　Detecting a lung cancer-associated transcript in a cell from a patient
PT　for treating lung cancer, by contacting a biological sample from the
PT　patient with a polynucleotide that exhibits increased or decreased
PT　expression in lung cancer.
XX
PS　Claim 22; Page 189; 453pp; English.
XX
CC　The invention relates to a method for detecting a lung cancer-associated
CC　transcript in a cell from a patient, comprising contacting a biological
CC　sample from the patient with a polynucleotide that selectively hybridises
CC　to a sequence that is at least 80 % identical to a gene that exhibits
CC　increased or decreased expression in lung cancer samples. Lung cancer-
CC　associated polynucleotides and polypeptides are used for identifying a
CC　compound that modulates a lung cancer-associated polypeptide, for
CC　inhibiting proliferation of a lung cancer-associated cell to treat lung
CC　cancer in a patient and for treating a mammal having lung cancer by
CC　administering a modulatory compound identified. The methods are useful
CC　for treating lung cancer, such as small cell lung cancer, non-small cell
CC　lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC　emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention.
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match   100.0%; Score 1522; DB 8; Length 1552;
Best Local Similarity   100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACAGTCAGCGACCGACATGGCTTCCCCGCTTCCCTCGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 ACAGTCAGCGACCGACATGGCTTCCCCGCTTCCCTCGTTGATCCCGGCC 90

Qy   61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTCCTCTTCTGATGCCCTGTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTTCGATGCCTGTCCAT 150

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGGCTCTTCTGGGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGGCTCTTCTGGGGAA 210

Qy   181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGATCACCCAGAGGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGATCACCCAGAGGAGGAGGAT 270

Qy   241 CCACCCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTACCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   271 CCACCCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy   301 GAAGTTAAGCCTAAATCAGGAGAAGAGAGGCTCCCTGAAGTTAGAGGATCTTACCTACTGTT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   331 GAAGTTAAGCCTAAATCAGGAGAAGAGAGGCTCCCTGAAGTTAGAGGATCTTACCTACTGTT 390

Qy   361 GAGGCTCCTGGAGAGATCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAGAGAGGGGAT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAGAGAGGGGAT 450

Qy   421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGCCTGGCCCCAGCCTGC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGCCTGGCCCCAGCCTGC 510

Qy   481 GCGGGCGCCGCCTTCCAGTCCCCGGTGGGATATCCGCCCCCCAGCTCGCCCGCTTCCGCCCCGCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCGGGCGCCGCCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCCGCTTCTCGCCCCGCC 570

Qy   541 CTGCGCCCCCTGGAACTCCTGGGGCTTCCAGTCTCCCCGGCCTCCCGGCCTGCCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 CTGCGCCCCCTGGAACTCCTGGGGCTTCCAGTCTCCCCGGCCTCCCGGCCTGCCC 630

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGGGGCGCTCCCTGCCTGGGGTCCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 AACAATGGCCACAGTGTGCAACTGACCCTGGGGCGCTAGAGATGGCCTCGGGGTCC 690

Qy   661 GGGCGGCGGAGTACCGGGGCTTCTGCAGCTGCATCTGGGGGGCGGCTGCTCAGGTCGTCTCCCGGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 GGGCGGCGGAGTACCGGGGCTGCGACCTCGCATCTGCACTGGGGCTGCAGGTCGTCCGGC 750

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTCCGAGATCCACGTGGTTCACCTCAGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTCCGAGATCCACGTGGTTCACCTCAGC 810

Qy   781 ACCGCCCTTTGCCAGAGTTGACGAGGGCCCTGGCCGTGTTGGCC 840
          ||||||||||||||||||||||||||||||||||||||||||||
Db   811 ACCGCCCTTTGCCAGAGTTGACGAGGGCCTGGCCGTGTTGGGC 870

Qy   841 GCCCTTTCTGGAGGAGGAGGGGCCCGGGAAGAAAAAACAGTCCTATGAGCAGTTGCTGTCTCGCTTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 GCCTTTCTCTGGAGGAGGAGGGGCCCGGGAAGAAAAAACAGTCGGTTGCTGTGTCTGCTTG 930

Qy   901 GAAGAAAATGGCTGAGGAAGGCTCAGGAGACTCAGAGTCCCAGGACTGAACTTGCAGGCTGACTC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 GAAGAAAATCGGCTGAGGAAGGCTCAGGAGACTCAGAGTCCCAGGACTGGACTGAGGACCATATCTGCACTC 990

Qy   961 CTGCCCCTTGGACTTCAGCCCGGCCTACTTCCAATATGAGGGGTTCTTCGACTCAGGGGTTGGCTTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CTGCCCCTTCGACTTCAGCCCGCCCTACTTCCAATATGAGGGTTCTTCTGACTCAGACTTGT 1050

Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACACAGTGGATGCTGAGGTGCTAAGCAGGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGAGTGATGCTGAGGTGCTAAGCAGGTC 1110

Qy   1081 CACACCCTCTCTGACACCCCTGTGCGGGACCTGGTGCTGGGGACTTCCGGCTACAGCTGAACTTCCGA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 CACACCCTCTCTGACACCCCTGTGGGGACCTGGTGGACTCTCGGCTACAGCTGAACTTCCGA 1170

Qy   1141 GCGACGGCAGCGCCTTGAAATGGGGCGGAGTGATTGAGGGGCTCCTTCCCCCTGCCAGGCAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 GCGACGGCAGCGCCTTGAAATGGGCGGAGTGATTGAGGGGCTCCTTCCCCTGCCTGAGTGGACAGC 1230

Qy   1201 AGTCCTTCGGCGGCTCGTGGAGCCAGTCCAGCTGAGCTCGCTGCTGGGCCTGGCCTGGCTGGTGACATCCTA 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 AGTCCTTCGGCGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGGCCTGCTGGTGACATCCTA 1290

Qy   1261 GCCCTGGTTTTTTGGCCTCCTCTTTTTGCTGTCCACCAGCGTGGCGTTCCTTGTTCAGATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 GCCCTGGTTTTTTGGCCTCCTCTTTTCGCTGTCACCAGCGTCGCGGTTCCTTGTTCAGATGAGA 1350

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTTGAGCTAGAGAATGTGGAGAAGCCAGCAGAGGGCATCTGAGGG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AGGCAGCACAGAAGGGGAACCAAAGGGTGTTGAGCTACCGGCCCAGCGACAGAGGGTAGCCGAG 1410

Qy   1381 ACTGGAGCCTTAGAGCTGGATCTTGGAGAATGTGAGGAAGGCCAGCCAGAGGGCATCTGAGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ACTGGAGCCTTAGAGCCTGGATCTTGGAGAATGTGAGGAAGGCCAGCGATCTGAGGG 1470

Qy   1441 GGAGCCCGGTRAACTGTCCCTGTCCCTGCTCATTATTGCCACTCCTTTCTTTTTAACTGGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GGAGCCCGGTRAACTGTCCCTGTCCCTGCTCATTATTGGCACTTCTTTTTAAACTGGCCAAGAAATT 1530

Qy   1501 TTTAAAATAAAATATTTATAAT 1522
          ||||||||||||||||||||||
Db   1531 TTTAAAATAAAATATTTATAAT 1552

RESULT 12
ADG89343
ID   ADG89343 standard; DNA; 1552 BP.
XX
AC   ADG89343;
XX
DT   ADG89343;
XX
DT   11-MAR-2004 (first entry)
XX
DE   Cancer detection method related gene #6.
XX
KW   ds; cancer; gene expression;
KW   estrogen receptor-positive invasive breast cancer.
OS   Homo sapiens.
XX
PN   WO2003078662-A1.
XX
PD   25-SEP-2003.
XX
PF   12-MAR-2003; 2003WO-US007713.
XX
PR   13-MAR-2002; 2002US-0364890P.
PR   18-SEP-2002; 2002US-0412049P.
XX
PA   (GENO-) GENOMIC HEALTH INC.
XX
PI   Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX

WPI; 2003-767536/72.

DR
XX
PT Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.
XX
PS
XX
Disclosure; SEQ ID NO 291; 198pp; English.
XX
CC The invention relates to a method of predicting clinical outcome for a
CC patient diagnosed with cancer by determining the expression level of one
CC or more genes, or their expression products, selected from p53BP2,
CC cathepsin B, cathepsin L, Ki67/MIB1, and thymidine kinase in a cancer
CC tissue obtained from the patient, normalized against control gene(s), and
CC compared to the amount found in a reference cancer tissue set. The
CC specification also discloses an array comprising polynucleotides
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-
CC 67, GSTM1, PR, BBC3, NME1, SURV, GATA3, TFRC, YB-1, DPYD, GSTM3, Ki-
CC RPS6KB1, Src, Chk1, ID1, EstR1, p27, CCNB1, XIAP, Chk2, CDC25B, IGF1R,
CC AK055699, P13KC2A, TGFB3, BAG1l, CYP3A4, EpCAM, VEGFC, pS2, hENT1, WISP1,
CC HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFIA,
CC CDH1, HIF1t, IGFBP3, CTSB, Her2 and DIABLO, immobilized on a solid
CC surface. The methods are useful for predicting clinical outcome for a
CC patient diagnosed with cancer, classifying cancer, and predicting the
CC likelihood of long-term survival of a breast cancer or a patient
CC diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC positive invasive breast cancer. This sequence corresponds to a gene
CC sequence whose expression is detected by the method of the invention.
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match   100.0%; Score 1552; DB 10; Length 1552;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 ACAGTCAGCCGCCATGGCTTCCCCTGCCCCCTGGCCTCCCTCCTTCTGTTGATCCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ACAGTCAGCCGCCATGGCTTCCCCTGCCCCCTGGCCTCCCTCCTTCTGTTGATCCCGGCC 90

Qy         61 CCTGCTCCAGGGCCTCACTGCTGCTGTCACTGTCACTGTCCCCAGCCCTGGGGGGGGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CCTGCTCCAGGGCCTCACTGCTGCTGTCACTGTCACTGTCCCCAGCCCTGGGGGGGGGC 150

Qy        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCCTTGGGGAGGCTCTTCTCTGGGGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCCTTGGGGAGGCTCTTCTCTGGGGAA 210

Qy        181 GATGACCCACTCGGGCGAGGGGAGGGATCTCCCAGTGAAGGAGGAATTCACCCAGAGGAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GATGACCCACTCGGGCGAGGGGAGGGATCTCCCAGTGAAGGAGGAATTCACCCAGAGGAGGAT 270

Qy        241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCT 330

Qy        301 GAAGTTAAGCCTAAATCAGAGAAGAGAGGGCCTCCCTGAAGTTAGAGAGATCTACCTACTTGTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GAAGTTAAGCCTAAATCAGAGAAGAGAGGGCCTCCCTGAAGTTAGAGAGATCTACCTACTTGTT 390

Qy        361 GAGGCTTCCTGGGAGATCCTCAAGAACCCCAGAGAATAATGGCCACAGGGGACAAAGAGAGGGGAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GAGGCTTCCTGGGAGATCCTCAAGAACCCCAGAGAATAATGGCCACAGGGGACAAAGAGAGGGGAT 450

Qy        421 GACCAGAGTCATTGGGCGGCGTATGGAGGGGACCCCGGCCCCTGGCCCCGGGGTGTCCCCAGCCTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GACCAGAGTCATTGGGCGGCGTATGGAGGGGACCCCGGCCCCTGGCCCCGGGGTGTCCCCAGCCTGC 510

Qy        481 GCGGGGCCGCCCTTCCAGTCCCCGGTGGGATAATCCGCGCGCCGGCCCCCGGCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GCGGGGCCGCCCTTCCAGTCCCCGGTGGGATAATCCGCGCGCCGGCCCCCGGCC 570

Qy        541 CTGGCGCCCCCTGGAACTTCCTGGGCTTCCAGTCGCGCCTCGGCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTGGCGCCCCCTGGAACTTCCTGGGCTTCCAGTCGCGCCTCGGCC 630

Qy        601 AACAAATGGGCCACAGTGTGCAACTGAACTGACCCTGCCCTTCCTCCCTTGCCCTCCCTCCTTGGGGTTCCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 AACAAATGGGCCACAGTGTGCAACTGAACTGACCCTGCCCTTCCTCCCTTGCCCTCCCTCCTTGGGGTTCCC 690

Qy        661 GGGGCGGGGGAGTACCCGGGCCTCTGCAGCTGCATCTGCAGCTGCACTGGGGGGGGGGGGCTAGAGATGGCTCTTCCGGGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GGGGCGGGGGAGTACCCGGGCCTCTGCAGCTGCATCTGCAGCTGCACTGGGGGGGGGGGGCTAGAGATGGCTCTTCCGGGGC 750

Qy        721 TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGACTGCACTGACCCTGCCTCCTGCCTTCTGGGGGGGGGGTCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGACTGCACTGACCCTGCCTCCTGCCTTCTGGGGGGGGGTCCC 810

Qy        781 ACCCGCCTTGCCAGAGTTGACGAGGAGGCCCTTGGGGCTGCCCGGCGCCGCGGGGGGCGGAGGCCCTGCCGGGTGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 ACCCGCCTTTGCCAGAGTTGACGAGGAGGCCCTTGGGGCTGCCCGGCGCCGCGGGGGGCGGAGGCCCTGCCGGGTGCCC 870

Qy        841 GCCTTTCTCTGGAGCAGGGCCCCGGCGAAGAAAACAGTGCCTTATGAGCAGTTGCTTGCTGTCTCGCTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 GCCTTTCTCTGGAGCAGGGCCCCGGCGAAGAAAACAGTGCCTATGAGCAGTTGCTTGCTGTCTCGCTTG 930

Qy        901 GAAGAAAATGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATAATATCTGCACTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 GAAGAAAATGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATAATATCTGCACTC 990

Qy        961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCCCGT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCCCGT 1050

Qy       1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACAGTGAATGCTGAGTCCTAAGCAGCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACAGTGAATGCTGAGTCCTAAGCAGCTC 1110

Qy       1081 CACACCCTTCTCTGACACCCGTGTGGGGGACCTGGGTGACTCTCGGCGTACAGCTGAACTTCCGA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 CACACCCTTCTCTGACACCCGTGTGGGGGACCTGGGTGACTCTCGGCGTACAGCTGAACTTCCGA 1170

Qy       1141 GCGACGCAGCCCTTTGAATGGGCAGGTGATTGAGGCCCTCCTTCCCTTCCTGCTGGAGTGGGACAGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GCGACGCAGCCCTTTGAATGGGCAGGTGATTGAGGCCCTCCTTCCCTTCCTGCTGGAGTGGGACAGC 1230

Qy       1201 AGTCCTCGGGGCGTCGCAGCCAGTCCAGCTGAATTCCTGGGCCTCTGGAGTGGTGATCCTA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 AGTCCTCGGGGCGTCGCAGCCAGTCCAGCTGAATTCCTGGGCCTCTGGAGTGGTGACATCCTA 1290

Qy       1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGGCGTCGCGGTTCCTTGCTGTGCAGATGAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGGCGTCGCGGTTCCTTGCTGTGCAGATGAGA 1350

Qy       1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTGAGCTGAGCGTAGCCGAGGTAGCCGAG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTGAGCTGAGCGTAGCCGAGGTAGCCGAG 1410

Qy       1381 ACTGGAGCCTAGAGGCCTGGATCTGGAGAAATGTGAGGAAGCCAGAGGCACTCTGAGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 ACTGGAGCCTAGAGGCCTGGATCTTGGAGAAATGTGAGGAAGCCAGAGGCACTCTGAGGG 1470

Qy       1441 GGAGCGCCGGTAACTGTCTCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GGAGCGCCGGTAACTGTCCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530

Qy       1501 TTTTAAAATAAATATTTTATAAT 1522
              |||||||||||||||||||||||
Db       1531 TTTTAAAATAAATATTTTATAAT 1552
```

RESULT 13
ACC72730
ID ACC72730 standard; cDNA; 1552 BP.
XX
AC ACC72730;
XX
DT 09-JUL-2003 (first entry)

```
DE   Human cancer related protein encoding cDNA SEQ ID NO:69.
XX
KW   Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW   heart disease; atherosclerosis; endometriosis; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200305138-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-US029560.
XX
PR   17-SEP-2001; 2001US-0334690P.
PR   20-SEP-2001; 2001US-0323887P.
PR   13-NOV-2001; 2001US-0350666P.
PR   08-FEB-2002; 2002US-0355145P.
PR   08-FEB-2002; 2002US-0355257P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI   Zlotnik A;
XX
DR   WPI; 2003-354600/33.
DR   P-PSDB; ABR58595.
XX
PT   New genes that are up-regulated or down-regulated in cancers, useful as
PT   markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT   therapeutic targets for screening drugs for treating these diseases.
XX
PS   Claim 8; Page 662; 767pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   comprises the sequence of any of the genes that are up-regulated or down-
CC   regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC   acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC   related gene nucleotide sequences which encode the proteins given in
CC   ABR58521 to ABR58709. Also described: (1) determining the presence or
CC   absence of a pathological cell in a patient; (2) an expression vector
CC   comprising a nucleic acid molecule described above; (3) a host cell
CC   comprising the vector; (4) an isolated polypeptide, which is encoded by
CC   the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC   of (4); (6) specifically targeting a compound to a pathological cell in a
CC   patient by administering to the patient the antibody above; and (7) a
CC   drug screening assay. The nucleic acid is useful as diagnostic markers or
CC   therapeutic targets. In particular, the nucleic acid is useful for
CC   diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC   bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC   pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC   atherosclerosis and endometriosis. The nucleic acid is also useful in
CC   drug screening, particularly for identifying agents for treating these
CC   pathologies
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1522;  DB 10;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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```
Qy         1 ACAGTCAGCGCCATGGCTCCCTCTGTGCCCAGCACCCGGCC                                      60
             ||||||||||||||||||||||||||||||||||||||||
Db        31 ACAGTCAGCGCCATGGCTCCCCTCTGTGCCCAGCACCCGGCC                                     90

Qy        61 CCTTGGCTCAGGCCTCACTCGTGCTGTGCTGCTCTGCTTCTCACTGTGCTCGTCTCCAT                    120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        91 CCTGCTCCAGGCCTCACTCGTGCTGTGCTGCTCTGCTTCTCGATGCCTGTCCAT                         150

Qy       121 CCCCAGAGGTTGCCCGGATGCAGGAGGAGGAATTCCCCCTTGGGGAGGAGGCTCTCTGGGGAA               180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       151 CCCCAGAGGGTTGCCCGGATGCAGGAGGGATTCCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA               210

Qy       181 GATGACCCACTGGGCGGGAGGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT            240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       211 GATGACCCACTGGGCGGGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT            270

Qy       241 CCACCCCGGAGGAGGAGGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT             300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       271 CCACCCCGGAGGAGGAGGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT             330

Qy       301 GCGGGTAAGCCTAAAATCAGAGAGAGAGAGGGCTCCCTGAAGTTAGAGGATCTACTGTT               360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       331 GAAGTTAAGCCTAAAATCAGAGAGAGAGAGGGCTCCCTGAAGTTAGAGGATCTACTGTT               390

Qy       361 GAAGGGCTCCTGGAGGAATCCTCAAGGAACCCCCAGAATAATGCCCACACAGGGACAAAAGAAGGGAT     420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       391 GAAGGGCTCCTGGAGGATCCTCAAGGAACCCCCAGAATAATGCCCACACAGGGACAAAAGAAGGGAT     450

Qy       421 GACCAGAGTCATTGGGCGTATGGAGGCGACCCGGCCCCCGGGTGTCCCAGCCTGC          480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       451 GACCAGAGTCATTGGGCGTATGGAGGCGACCCGGCCCCCGGGTGTCCCAGCCTGC          510

Qy       481 GCGGCGCCGCTTCCCAGTCCCGGGTTGGATATCCGGCCCCCCAGCGTCGCGCGGCCCTTCTGCCCGCCGCC     540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       511 GCGGGCGCCGCTTCCCAGTCCCGGGTTGGATATCCGGCCCCCCAGCGTCGCGCGGCCCTTCTGCCCGCCGCC     570

Qy       541 CTGCGCCCCCCTGGAACTCTGGGCTTCCAGCTCCCCCGGTCGCCCCCGCCCCCCCAGAACTGCGCCCCGGC   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       571 CTGCGCCCCCCTGGAACTCTGGGCTTCCAGCTCCCCCGGTCGCCCCCGCCCCCCCAGAACTGCGCGCGC      630

Qy       601 AACAATGGCACAGTGTGCAACTGACCCTGCCTCCTGGGCGCTAGAGATGGGCTCTGGGTCCC           660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       631 AACAATGGCACAGTGTGCAACTGACCCTGCCTCCTGGGCGCTAGAGATGGGCTCTGGGTCCC           690

Qy       661 GGGCGCGGGAGTACCGGCGGCTCTGCAGCTGCAGCTCGCACTGCAGTGCGGGTTCGTTCCTGGGGC         720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       691 GGGCGCGGGAGTACCGGCGGCTCTGCAGCTGCAGCTCGCACTGCAGTGCGGGTTCGTTCCTGGGGC         750

Qy       721 TCGGGAGCACTGTGGAAGGCCACCGTTCCCTGCGAGGATCCAGGTGGTTCACCTCAGC               780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       751 TCGGGAGCACTGTGGAAGGCCACCGTTCCCTGCGAGGATCCAGGTGGTTCACCTCAGC               810

Qy       781 ACCGGCCTTTCCCAGACGTTGACGAGGCCCTTGGGGCCGGAGCCGGCTGGGCGTGGTTGGGCC          840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       811 ACCGGCCTTTCGCCAGACGTTGACGAGGCCCTTGGGGCCGGAGCCGGCTGGGCGTGGTTGGGGCC         870

Qy       841 GCCCTTTCTGGAGGAGGGCCCGGAGAAAAACAGTGGCCTATGAGCAGTGCTTGCTGTCTCGCTTG        900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       871 GCCCTTTCTGGAGGAGGGCCCGGAGAAAAACAGTGGCCTATGAGCAGTGCTGTCTCGCTTG         930

Qy       901 GAAGGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGAGACTGGAGCATATCTGCACTC         960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       931 GAAGGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGAGACTGGACATATCTGCACTC         990

Qy       961 CTGCGCCTCTCGACTTCAGCCCGCTACTTCCAATATGAGGGGGTCTCTGGACTCACGCCCTGT       1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       991 CTGCGCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTGACTACACGCCCTGT       1050

Qy      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAATGCTGGACAGAGCTC        1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAATGCTGGACAGAGCTC        1110

Qy      1081 CACACCCTCTCTGACACCCTGGTGGGGGACCTGGACTCTGGGCTAGACTCAGCTGAACTTCCGA      1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1111 CACACCCTCTCTGACACCCTGGTGGGGGACCTGGACTCTGGGCTAGACTCAGCTGAACTTCCGA      1170

Qy      1141 GCGAGCGCAGCCTTTGGAATGGGCGAGTGATTGAGGGGCCTTCCCTTTCCCCTGCTGAAGCAGC      1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1171 GCGAGCGCAGCCTTTGGAATGGGCGAGTGATTGAGGGGCCTTCCCTTTCCCTGCTGGACAGC       1230

Qy      1201 AGTCCTTCGGCCTGCTGCTGGAGCCAGTCGACGCTGGAATTCCTGCCTGGCTTGTGCTGAGCATCCTA     1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1231 AGTCCTTCGGGCTGCTGCTGGAGCCAGTCGACGCTGGAATTCCTGCCTGGTGGTGCTGAGCATCCTA     1290
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Qy   1261 GCCCTCGGTTTTTTGGCCTCTTTTTTCGTTCCTTGTGCGTCGGCGTTCCTTGTGCGTCGCAGATGAGA 1320
Db   1291 GCCCTCGGTTTTTGCGCTCCTTTTTGTCGTCACCAGGGTGCGGTTCCTTGTGCGTCAGATGAGA 1350

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTAGCCGAG 1380
Db   1351 AGGCAGCACAGAAGGGGAACCAAAGGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTAGCCGAG 1410

Qy   1381 ACTCGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAACCAGCAGCCATCTGAGGG 1440
Db   1411 ACTCGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAACCAGCAGCCATCTGAGGG 1470

Qy   1441 GGAGCCGGTAACTGTCCTGTCCTCATTATGCCACTTCCTTTTAACTGGCCAAGAAATT 1500
Db   1471 GGACCCGGTAACTGTCCTGTCCTCATTATGCCACTTCCTTTTAACTGGCCAAGAAATT 1530

Qy   1501 TTTTAAAATAAATATATTTATAAT 1522
Db   1531 TTTTAAAATAAATATATTTATAAT 1552
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RESULT 14
ID   AB277284   standard; cDNA; 1552 BP.
XX
AC   AB277284;
XX
DT   28-MAY-2003   (first entry)
XX
DE   Nucleotide sequence of human CA9 polypeptide.
XX
KW   Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
KW   microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
KW   follicular development; CA9; HXB; IGFBP5; HPARP; STC1; mig-6; SSR4;
KW   cancer; gene; 88.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             43..1422
FT                   /tag= a
FT                   /product= "CA9"
XX
PN   WO200301025-A1.
XX
PD   06-FEB-2003.
XX
PF   26-JUL-2002; 2002WO-US023786.
XX
PR   26-JUL-2001; 2001US-0307600P.
PR   24-JUL-2002; 2002US-00201642.
XX
PA   (UYDU-) UNIV DUKE MEDICAL CENT.
XX
PI   Riggins GJ, Lal A;
XX
DR   WPI; 2003-239423/23.
DR   P-PSDB; ABP99744.
XX
PT   Inhibiting angiogenesis for treating wound healing, retinopathy,
PT   ischemia, inflammation, microvasculopathy, bone healing, skin
PT   inflammation or follicular development by providing to a subject an
PT   antisense polynucleotide.
XX
PS   Claim 1; Page 47; 66pp; English.
XX
CC   The present sequence encodes a human CA9 polypeptide. It is used in the
CC   method of the invention. The specification describes a method modulating
CC   angiogenesis associated with wound healing, retinopathy, ischemia,
CC   inflammation, microvasculopathy, bone healing, skin inflammation or
CC   follicular development. The method comprises providing to a subject HOG3,
CC   HOG8, HOG18, CA9, HXB, IGFBP5, HPARP, STC1, mig-6 or SSR4. The methods,
CC   antisense polynucleotides, polypeptides and antibodies are useful for
CC   treating wound healing, retinopathy, ischemia, inflammation,
CC   microvasculopathy, bone healing, skin inflammation or follicular
CC   development, or cancer such as breast, colon or lung cancer, or
CC   glioblastoma
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match          100.0%;   Score 1522;   DB 10;   Length 1552;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 ACAGTCAGCGCACATGGCTCCCCTCCGTTCCCGTTCCCTCCTCGTTTCGTTTGTTGGTCCCGGGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTCAGCGCACATGGCTCCCCTCCGTTCCCGTTCCCTCCTCGTTTCGTTTGTTGGTCCCGGGCC 90

Qy     61 CCTGCTCCAGGCCCTCACTGTCCAACTGCTTGCTGTCTGCTCCTGTTCACTGGCCTGCTTCCAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGCCCTCACTGTCCAACTGCTTGCTGTCTGCTCCTGTTCACTGGCCTGCTTCCAT 150

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCCTTGGGAGGAGGCTCTTCTTTGGGGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCCTTGGGAGGAGGCTCTTCTTTGGGGAA 210

Qy    181 GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGGATTCACCCAGAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGGATTCACCCAGAGAGGAGGAT 270

Qy    241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCGGAGAGGAGGAGGATCTACCTGGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAAATCAGAAGAGAGAGGCTCCCTGGAGGTTAGAGGATCTTACCTTACTGTT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAAATCAGAAGAGAGAGGCTCCCTGGAGGTTAGAGGATCTTACCTTACTGTT 390

Qy    361 GAGGCTCCTGGAGAGTCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAGAAGGGGAT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GAGGCTCCTGGAGAGTCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy    421 GACCAGAGTCATTGGGCGGCTTAGGAGGCACCCCAGGGCCGCCCCTGGGCCGCCCCTGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 GACCAGAGTCATTGGGCGGCTTAGGAGGCACCCCAGGGCCGCCCCTGGGCCGCCCCTGC 510

Qy    481 GCGGGCCGCGCCTTCCAGTCCCCGGGTGGATATCCGGCCCCAGCTCGCCCGCCTTCTGCCCGCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GCGGGCCGCGCCTTCCAGTCCCCGGGTGGATATCCGGCCCCAGCTCGCCCGCCTTCTGCCCGCC 570

Qy    541 CTGCGCCCCCTGGAACTCCTCGGGCTTCCAGCTCCCGGGCCGCTCCCAGACTGCGCCCGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 CTGCGCCCCCTGGAACTCCTCGGGCTTCCAGCTCCCGGGCCGCTCCCAGACTGCGCCCGCC 630

Qy    601 AACAATGGCCACAGTGTGCCAACTGACCCTGCCCTCCTCGGGCTAGGAGGCTCGGGGTCCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 AACAATGGCCACAGTGTGCCAACTGACCCTGCCCTCCTCGGGCTAGGAGGCTCGGGGTCCC 690

Qy    661 GGGCGGGGAGTACCGGGGCTCTCGAGCTGCATCTGCACTGGGGCTGCAGGTCGTCCGGGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 GGGCGGGGAGTACCGGGGCTCTCGAGCTGCATCTGCACTGGGGCTGCAGGTCGTCCGGGC 750

Qy    721 TCGGAGCACACTGTGGAAGGGCACCGTTCCCGAGATCCAGCTTCCAGCTTCACCCTCAGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCGGAGCACACTGTGGAAGGGCACCGTTCCCGAGATCCAGCTTCCAGCTTCACCCTCAGC 810

Qy    781 ACCGGCCTTTGCCCAGAGTTGACGGAGGCCTTGGGGGCGCCGGCCTTGGGCCGTGTTCGGCC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ACCGGCCTTTGCCCAGAGTTGACGGAGGCCTTGGGGGCGCCGGCCTTGGGCCGTGTTCGGCC 870

Qy    841 GCCTTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTTGCCTATGAGCAGTTGCTGCGTCCGGCTTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTTGCCTATGAGCAGTTGCTGCGTCCGGCTTG 930

Qy    901 GAAGAAATCGCTCGAGGAGGCTCAGGACTCAGGTCCCAGAGACTCAGCATATCTGCACTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931
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Db    931  GAAGAAATGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC  990
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Qy    961  CTGCCCCTGGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTTGACTTACACCGCCCCTGT 1020
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Db    991  CTGCCCCTGGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTTGACTTACACCGCCCCTGT 1050

Qy   1021  GCCCAGGGTGTCATCTGACTGTGTTTAACCACAACAGTGATGCTGAGTGCTAAGCAGCTC 1080
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Db   1081  CACACCCCTCTCTGACACACCCTGTGGGGGATCTGGCTCGGTGAGTCTCGGCTTACAGCG 1140
Db   1111  CACACCCTCTCTGACACACCCTGTGGGGGAACCTGGGTGACTCTCAGCACTTCACAGCG 1170

Qy   1141  GCGACGCAGCAGCCTTTGAAATGGGCGGAGTGATTGAGTGATTGAGGCCTCCTTCCCTGGCTGGAGTGGACAGC 1200
Qy   1171  GCGACGCAGCAGCCTTTGAAATGGGCGGAGTGATTGAGGCCTCCTTCCCTGGCTGGAGTGGACAGC 1230

Db   1201  AGTCCTCGGGCTTCTGACCCAGTCCAGTGAGTTCCTGCCTGGTCTGGTGACATCCTA 1260
Db   1231  AGTCCTCGGGCTTCTGACCCAGTCCAGTGAGTTCCTGCCTGGTCTGGTGACATCCTA 1290

Qy   1261  GCCCTGGTTGTTTTTGGGCTTCCTTTTTTTTGGCTTCACCAGGCGTGGGTTCCTTGTGTCAGATGAGA 1320
Db   1291  GCCCTGGTTGTTTTTGGGCCTCCTTTTTTTTGGCTTCACCAGGCGTGTGCGGTTCCTTGTGTCAGATGAGA 1350

Qy   1321  AGGCAGCACAGAGAGGGGGAACCAAAAGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTTAGCCGAG 1380
Db   1351  AGGCAGCACAGAGAGGGGGAACCAAAAGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTTAGCCGAG 1410

Db   1381  ACTGGAGCCTAGAGGCTTGGATCTTGGAGAAATGTGAGAGGCCCACCCAGAGGGGCATCTGAGGG 1440
Db   1411  ACTGGAGCCTAGAGCTGGATCTTGGAGAATGTGAGAGAACCCAGCCAGAGGCATCTGAGGG 1470

Qy   1441  GGAGCCGGTAACTGTCTCGTCTCATTAATGCCAACTTCCTTTTAACTGCCAAGAAATT 1500
Db   1471  GGAGCCGGTAACTGTCTCGTCTCATTAATGCCAACTTCCTTTTAACTGCCAAGAAATT 1530

Qy   1501  TTTTAAAATAAATATTTTATAAT 1522
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Db   1531  TTTTAAAATAAATATTTTATAAT 1552
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RESULT 15
ADN39704

ID   ADN39704 standard; cDNA; 1552 BP.
XX
AC   ADN39704;
XX
DT   17-JUN-2004 (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C76.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularisation syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cyostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-03506066P.
PR   21-NOV-2001; 2001US-03324464P.
PR   29-NOV-2001; 2001US-03343993P.
PR   03-DEC-2001; 2001US-0335394P.

PR   14-DEC-2001; 2001US-03403076P.
PR   08-JAN-2002; 2002US-03472011P.
PR   10-JAN-2002; 2002US-03473049P.
PR   08-FEB-2002; 2002US-03552250P.
PR   13-FEB-2002; 2002US-03567147P.
PR   20-FEB-2002; 2002US-03550777P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-03701107P.
PR   12-APR-2002; 2002US-03722467P.
PR   05-JUN-2002; 2002US-03866147P.
PR   16-JUL-2002; 2002US-03968397P.
PR   22-JUL-2002; 2002US-03977775P.
PR   22-JUL-2002; 2002US-03978452P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI   Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   P-PSDB; ADN39921.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 8; SEQ ID NO C76; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN36683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularisation syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match   100.0%; Score 1522; DB 11; Length 1552;
Best Local Similarity   100.0%;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1  ACAGTCAGCCGCATGGCTCCCCGTGCCCAGCCCCTGGCTCCCCTCTGTTGATCCGGCC  60
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Db     1  ACAGTCAGCCGCATGGCTCCCCGTGCCCAGCCCCTGGCTCCCCTCTGTTGATCCCGGCC  90

Qy    31  CCTTGCTCCAGGCCCTCACACTGCTCAACTGCTGCTCTGCTTCTTCGATGCCCTGTCCAT 120
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Qy    61  CCTTGCTCCAGGCCCTCACACTGCTCAACTGCTGCTCTGCTTCTTCGATGCCCTGTCCAT 120

Db    61  CCTGCTCCAGGCCCTCACTGCTCAACTGCTGCTTCTGCTGCCCTTCTGATGCCCTGTCCAT 150

Qy    91  CCTGCTCCAGGCCCTCACTGCTCAACTGCTGCTTCTGCTGCCCTTCTGATGCCCTGTCCAT 150

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Qy   121  CCCCAGAGGTTGCCCCGGATGCGAGGAGGATTCCCCCTGGGGAGGAGGCTCTTTCTGGGGAA 180

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Qy   151  CCCCAGAGGTTGCCCCGGATGCGAGGAGGATTCCCCCTGGGGAGGAGGCTCTTTCTGGGGAA 210

Db   151  CCCCAGAGGTTGCCCCGGATGCGAGGAGGATTCCCCCTGGGGAGGAGGCTCTTTCTGGGGAA 210

Qy   181  GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 240

Db   181  GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 270

Qy   211  GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 270

Db   211  GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 270

Qy   241  CCACCCCGGAGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGAGGAGGATCTACCT 300

Db   241  CCACCCCGGAGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGAGGAGGATCTACCT 300

Qy   271  CCACCCCGGAGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGAGGAGGATCTACCT 330
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Qy    301 GAAGTTAAGCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT  360
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Db    331 GAAGTTAAGCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT  390

Qy    361 GAGGCTCCTGGAGATCCTCAAGACACCCAGAATAAATGCCCACAGGAACAAAGAAGGGGAT   420
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Db    391 GAGGCTCCTGGAGATCCTCAAGACACCCAGAATAAATGCCCACAGGAACAAAGAAGGGGAT   450

Qy    421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGGCCCTTGCCCCGGCGTCCCCCAGCCTTGC   480
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Db    451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGGCCCTTGCCCCGGCGTCCCCCAGCCTGC   510

Qy    481 GCGGGCCGGCTTCCAGTCCCCGGTGGAATATCCGCCCCCAGCTCGGCCGCCCTTCTGCCCGGCC   540
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Qy    541 CTGCGGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCGCCTCCCAGAACTGCCCCTGCGCC   600
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Qy    601 AACAATGGGCCACAGTGTGCAAACTGACCCCTGCCTTCCTGGCTAGAGATGGCTCTGGGTCC   660
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Qy    661 GGGCGGGAGTACCGGGCTCTGCAGCTGCCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC   720
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Db    691 GGGCGGGGAGTACCGGGCTCTGCAGCTGCCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC   750

Qy    721 TCGGAGCACACTGTGGAAGGCCACCCGTTTCCCTGCCGGAGATCCACGTGGTTCACCTCAGC   780
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Db    751 TCGGAGCACACTGTGGAAGGCCACCCGTTTCCCTGCCGGAGATCCACGTGGTTCACCTCAGC   810

Qy    781 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGGCGCCCGGGAGGCCTGGCCGTGTTGCC   840
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Db    811 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGGCGCCCGGGAGGCCTGGCCGTGTTGCC   870

Qy    841 GCCTTTCTGGAGGAGGCCCCGGAGAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG   900
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Db    871 GCCTTTCTGGAGGAGGCCCCGGAAGAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG   930

Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACACATATCTGCACTC   960
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Qy    961 CTGCCCTCTGACTTCAGCCGCTACTTCCCAAATATGAGGGGTCTCTGACTACACCGCCCTGT  1020
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Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTGTTTAACCAGACAGTGATGCTGAGTGGCTAAGCAGCTC  1080
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Qy   1081 CACACCCCTCTCTGACACCCTGTGGGGACCTGGTCGACTCTGACTGGCTACAGCTGAACTTCCGA  1140
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Qy   1141 GCCGACGCAGCCTTTGAATGGGCCAGGCCTCCTTCCCTGCTGGAGTGGACAGC  1200
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Db   1171 GGCAGCGCAGCCTTTGAATGGGCCAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC  1230

Qy   1201 AGTCCTCGGGCGCTGCTGAGCCAGTCCCAGCTGAATTCCTGCCCTGGCTGCTGACATCCTA  1260
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Db   1231 AGTCCTCGGGCTGCTGAGCCAGTGATTCCTGCCCTGGCTGCTGACATCCTA  1290

Qy   1261 GCCCTGGTTTTTTGGCCTCCTTCTTTTGCGTGTCACCAGGGGTTCCTTGTTGCGAGATGAGA  1320
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Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGGTGTGAGCTACCGGCCTAGCCGAG  1380
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OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:          February 6, 2005, 07:18:21 ; Search time 154 Seconds
                                             (without alignments)
                                             7024.810 Million cell updates/sec

Title:           US-09-967-237A-1
Perfect score:   1522
Sequence:        1 acagtcagcgccgcatggctcc............ttaaaataatattatat 1522

Scoring table:   OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0
Searched:        824507 seqs, 355394441 residues

Word size :      50

Total number of hits satisfying chosen parameters:      149

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :       Issued Patents NA:*
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                 3: /cgn2_6/ptodata/1/1na/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

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Result                        Query
No.     Score   Match  Length  DB    ID             Description
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  2     1522    100.0   1522    2    US-08-477-504A-1    Sequence 1, Appli
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  6     1522    100.0   1522    3    US-08-487-077A-1    Sequence 1, Appli
  7     1522    100.0   1522    3    US-08-485-863A-1    Sequence 1, Appli
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 19     365     24.0   10898    2    US-08-477-504A-5    Sequence 5, Appl
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 21     365     24.0   10898    2    US-08-485-862B-5    Sequence 5, Appl
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 24     365     24.0   10898    3    US-08-485-049D-5    Sequence 5, Appli
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 43     191     12.5    191     2    US-08-485-862B-38   Sequence 38, Appl
 44     191     12.5    191     3    US-08-787-739-38    Sequence 38, Appl
 45     191     12.5    191     3    US-08-487-077A-38   Sequence 38, Appl
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                              ALIGNMENTS

RESULT 1
US-08-481-658B-1
; Sequence 1, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT: Pastorekova, Silvia
;  APPLICANT: Pastorek, Jaromir
;  TITLE OF INVENTION: MN Gene and Protein
;  NUMBER OF SEQUENCES: 86
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Leona L. Lauder
;  STREET: 6 Mariposa Court
;  CITY: Tiburon
;  STATE: California
;  COUNTRY: USA
;  ZIP: 94920
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/481,658B
;  FILING DATE: 07-JUN-1995
;  CLASSIFICATION: 424
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/260,190
;  FILING DATE: 15-JUN-1994
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Lauder, Leona L.
;  REGISTRATION NUMBER: 30,863
;  REFERENCE/DOCKET NUMBER: D-0021.3E
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 415-435-2034
;  TELEFAX: 415-435-0727
;  INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 1522 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
US-08-481-658B-1

  Query Match             100.0%;  Score 1522;  DB 2;  Length 1522;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy      1 ACAGTTCAGCGCGCAATGGCTCCCCTGGCTCCCCAGCCCCTGGCTCCCCTGTGTGCCCTGGCC 60
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Qy    181 GATGACACCCACTGGGCGGAGGATCTGCCCAGTGAAGAAGGATTCACCAGAGGAGGAGGAT 240
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Qy    421 GACCAGAGTCATTGGGCGTTATGGAGGCGACCCCGCCCCGGGGTGTTCCCCAGCCCTGC 480
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Db    421 GACCAGAGTCATTGGGCGTTATGGAGGCGACCCCGCCCCGGGGTGTTCCCCAGCCCTGC 480

Qy    481 GCGGGGCCGCCTTCCAGTCCCCGGTGGATATCCGCGCCCCAGCTCGCCGCCTTCTCGCCCCGGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGGCCGCTTCCAGTCCCCGGTGGATATCCGCGCCCCAGCTCGCCGCCTTCTCGCCCGGCC 540

Qy    541 CTGCGCGCCCCCTGGAAACTCCTGGGCCTTCCAGCTCCCAGAACTCGCCGCCCTGCGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGCGCGCCCCCTGGAAACTCCTGGGCTTCCAGCTCCCAGAACTGCGGCCCCTGCGC 600

Qy    601 AACAATGGCCACAGTGTGCCAACTGACCCTGCCTCCTGTGGTCTCTCGGGGTCCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACAATGGCCACAGTGTGCCAACTGACCCTGCCTCCTGGGTCTCTCGGGGGTCCC 660

Qy    661 GGGCGGGGAGTACCCGGGGCTCTCGCAGCTGCATCTCGCACTGGGGCTGCGTCCCGGGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGCGGGGAGTACCCGGGGCTCTCGCAGCTGCATCTCGCACTGGGGCTGCGTCCCGGGC 720

Qy    721 TCGGAGCACACTGTTGGGAAGGCCACCGTTTCCCTGCCGAGATCCAACGTGGTTCACCTCAGC 780
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Db    721 TCGGAGCACACTGTGGGAAGGCCACCGTTTCCCTGCCGAGATCCAACGTGGTTCACCTCAGC 780

Qy    781 ACCGCCCTTTGCCAGAGTTGACAGAGGCCCTTGGGGACGGCCTGGCCGTGGCCCGTGTTGGGCC 840
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Db    781 ACCGCCCTTTGCCAGAGTTGACAGAGGCCCTTGGGGACGGCCTGGCCGTGGCCCGTGTTGGGCC 840

Qy    841 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCCTATGAGGACAGTTGCTCGCTGCTCACTC 900
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Db    841 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCCTATGAGGACAGTTGCTCGTCGCTCACTC 900

Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGGGTCTCCAGGACTGGAGCATATCTGCACTC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAAGAAATCGCTGAGGAAGGCTCAGGGTCTCCAGGACTGGAGCATATCTGCACTC 960

Qy    961 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACGCCCTGT 1020
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Db    961 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACGCCCTGT 1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTCTGTGTTTAACCAGACACAGTGATGCTGATGCTGCTAAGCAGCTC 1080
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Qy   1081 CACACCCCTCTCGACACCCCTGTGGGGGACCTGGTGACTCTCGGGGCTACAGCTGAACTTCCGA 1140
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Db   1081 CACACCCCTCTCGACACCCCTGTGGGGGACCTGGTGACTCTCGGGGCTACAGCTGAACTTCCGA 1140

Qy   1141 GCGACGCAGCCCTTTGAATGGGCCGAGTGAGTTGAGGCTCCTCCTTCCCTTGCTTCCCTGCTGGAGTGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCCTTTGAATGGGCCGAGTGAGTTGAGGCTCCTCCTTCCCTTGCTTCCCTGCTGGAGTGGACAGC 1200

Qy   1201 AGTCCTCGGGCTGCTGAGCCCAGTCCAGCTGAATTCCTGCCCTGGCTCTGGGTGACATCCTA 1260
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Db   1201 AGTCCTCGGGCTGCTGAGCCCAGTCCAGCTGAATTCCTGCCCTGGCTCTGGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTTGTCACCAGCGGTCGCGGTTCCTTGTCAGATGAGA 1320
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Db   1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTTGTCACCAGCGGTCGCGGTTCCTTGTCAGATGAGA 1320

Qy   1321 AGGCAGCACAGGAGGGGAACCAAAGGGGGTGTTGTGAGCCTACCGCCACAGCACGAGGTAGCCCAG 1380
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Db   1321 AGGCAGCACAGGAGGGGAACCAAAGGGGGTGTTGTGAGCCTACCGCCACAGCACGAGGTAGCCCAG 1380

Qy   1381 ACTGGAGCCTAGGAGGCTGGGATCTTGGAGAAGTGTGGAGAAGGCCAGCCAGGAGGGCCATCTGAGGG 1440
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Db   1381 ACTGGAGCCTAGGAGGCTGGGATCTTGGAGAAGTGTGGAGAAGGCCAGCCAGGAGGGCCATCTGAGGG 1440

Qy   1441 GGAGCCGGTAACTGTCCCTGCTCCTCATTATGCCAACTTCCTTTTAACTGCCAAGAAATT 1500
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Db   1441 GGAGCCGGTAACTGTCCCTGCTCATTATGCCAACTTCCTTTTAACTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAAATAATTTTATAAT 1522
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Db   1501 TTTTAAAATAAAATAATTTTATAAT 1522
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RESULT 2
US-08-477-504A-1
Sequence 1, Application US/08477504A
Patent No. 5972353
; GENERAL INFORMATION:
;   APPLICANT: Zavada, Jan
;   APPLICANT: Pastorekova, Silvia
;   APPLICANT: Pastorek, Jaromir
;   TITLE OF INVENTION: MN Gene and Protein
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Leona L. Lauder
;     STREET: 6 Mariposa Court
;     CITY: Tiburon
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94920
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/477,504A
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/260,190
;     FILING DATE: 15-JUN-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Lauder, Leona L.
;     REGISTRATION NUMBER: 30,863
;     REFERENCE/DOCKET NUMBER: D-0021.3D
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-435-2034
;     TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1522 base pairs
;     TYPE: nucleic acid
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;
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
US-08-477-504A-1

Query Match      100.0%;  Score 1522;  DB 2;  Length 1522;
Best Local Similarity  100.0%;  Pred. No. 0;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 1522;  Conservative 0;

Qy     1 ACAGTCAGGCGCATGGCTCCCCGTGTGCCCCAGCCCCTGGTCTCCCTGTCTCTGTTGATCCCGGCC 60
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Db     1 ACAGTCAGGCGCATGGCTCCCCGTGTGCCCCAGCCCCTGGTCTCCCTGTCTCTGTTGATCCCGGCC 60

Qy    61 CCTGCTCCAGGCCTCACTGTGCAACTGTCCTGCTGTCACTGTGCTTCTGCTTCGAATGCCATTCGAT 120
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Db    61 CCTGCTCCAGGCCTCACTGTGCAACTGTCCTGCTGTCACTGTGCTTCTGCTTCGAATGCCATTCGAT 120

Qy   121 CCCCAGAGAGGTTGCCCCGGATGCACGGAGGATTCCCCCCTTGGGGAGAGGCTCTTCTCGGGGAA 180
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Db   121 CCCCAGAGAGGTTGCCCCGGATGCACGGAGGATTCCCCCCTTGGGGAGAGGCTCTTCTCGGGGAA 180

Qy   181 GATGACCCACTGGGGCGGAGGAGGATCTGCCCAGTGAAGAGAGATCTTACCT 240
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Db   181 GATGACCCACTGGGGCGGAGGAGGATCTGCCCAGTGAAGAGAGATCTTACCT 240

Qy   241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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Db   241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Qy   301 GAAGTTAAGCCTAAATCAGAAGAAGAGGCTCCCTGAAGTTAGGATCTACCTACTGTT 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAAGTTAAGCCTAAATCAGAAGAAGAGGCTCCCTGAAGTTAGGATCTACCTACTGTT 360

Qy   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAGAAGGGGAT 420
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Db   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAGAAGGGGAT 420

Qy   421 GACCAGAGTCATTGGCGCTATGGAGGGCCACCCCCCCGGGGTGTCCCCAGCCTGC 480
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Db   421 GACCAGAGTCATTGGCGCTATGGAGGGCCACCCCCCCGGGGTGTCCCCAGCCTGC 480

Qy   481 GCGGGGCCGCTTCCAGTCCCCGGTTGGATAATCCGGCCCTTCTCGCCCGCC 540
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Db   481 GCGGGGCCGCTTCCAGTCCCCGGTTGGATAATCCGGCCCTTCTCGCCCGCC 540

Qy   541 CTCGCGCCCCTGGAACTCCTGGGCGTTCCAGCTCCCAGACTGCGCGCCTGCGC 600
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Db   541 CTCGCGCCCCTGGAACTCCTGGGCGTTCCAGCTCCCAGACTGCGCGCCTGCGC 600

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCCTGCCCTCTGGGTCTCGGGGTCCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACAATGGCCACAGTGTGCAACTGACCCCTGCCCTCTGGGTCTCGGGGTCCC 660

Qy   661 GGGCGGGGAGTACCGGGCTCTGCACGTCGATCTGCACTGGGGCGGGCGTCGGTCCGGGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGGCGGGGAGTACCGGGCTCTGCACGTCGATCTGCACTGGGGCGGGCGTCGGTCCGGGC 720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCACTCGGTTCACCTCAGC 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCACTCGGTTCACCTCAGC 780

Qy   781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGCCCGGCCGGTCGTTGGCC 840
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Db   781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGCCCGGCCGGTCGTTGGCC 840

Qy   841 GCCTTTCTGGAGGAGGGGCCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTCTTCGCGCTTG 900
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Db   841 GCCTTTCTGGAGGAGGGGCCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTCTTCGCGCTTG 900

Qy   901 GAAGAAATCGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
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Db   901 GAAGAAATCGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy   961 CTGCCCCTTCGACTTCAGCCCGGCCTACTTCCAATATGAGGGGTCTTCTGACTACCGCCCTGT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CTGCCCCTTCGACTTCAGCCCGGCCTACTTCCAATATGAGGGGTCTTCTGACTACCGCCCTGT 1020

Qy  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGACAGTGATTGGGGGTTCTCAGACTGT 1080
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Db  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGACAGTGATTGGGGGTTCTCAGACTGT 1080

Qy  1081 CACACCCTCTCTGACACCCTGGGGGGACCTGGGTGACTCTGGGCTACAGCTGAACTTCCGA 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CACACCCTCTCTGACACCCTGGGGGGACCTGGGTGACTCTGGGCTACAGCTGAACTTCCGA 1140

Qy  1141 GCGACCGGCAGCCTTTGAAATGGGGCGAGGTGAGTTGAGTTGAGGGCTTCCTCTTCCCCGTCGTGGAGTGGACAGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCGACCGGCAGCCTTTGAAATGGGGCGAGGTGAGTTGAGTTGAGGGCTTCCTCTTCCCCGTCGTGGAGTGGACAGC 1200

Qy  1201 AGTTCCTTCGGGCGTCGTGCAGTCGCAGTCCAGCTGAATTCCTGCCTGCTGCTTCCTGCCACATCCTA 1260
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Db  1201 AGTTCCTTCGGGCGTCGTGCAGTCGCAGTCCAGCTGAATTCCTGCCTGCTGCTTCCTGCCACATCCTA 1260

Qy  1261 GCCCTGGTTTTTTGGGCCTCCTTTTTTGCCTGTCCACCAGGGTCGGGGTTCCTTGGTTGCAGATTGAGA 1320
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Db  1261 GCCCTGGTTTTTTGGGCCTCCTTTTTTGCCTGTCCACCAGGGTCGGGGTTCCTTGGTTGCAGATTGAGA 1320

Qy  1321 AGGCAGCACAGAAGGGGGACCAAAGGGGTGTGAGCTACCGCCCAGCAGCAGGAGGTAGCCGAG 1380
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Db  1321 AGGCAGCACAGAAGGGGGACCAAAGGGGTGTGAGCTACCGCCCAGCAGCAGGAGGTAGCCGAG 1380

Qy  1381 ACTCGAGCCCTTAGAGCCTGAGATCTTGGGAGAATGTGAGAAGCCAGCCAATGTGCCATCTGAGGG 1440
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Db  1381 ACTCGAGCCCTTAGAGCCTGAGATCTTGGGAGAATGTGAGAAGCCAGCCAATGTGCCATCTGAGGG 1440

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Db  1441 GGAGCCGGTAACTGTCCCTGTCCTGCTCATTATGCCACTTCCTTTTTAAACTGCCAAGAAATT 1500

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Db  1501 TTTTAAAATAAAATAATTTATATAAT 1522
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; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-0727
; TELEFAX: 415-435-2034
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-486-756A-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    181 GATGACCCACTCGGCGGAGGAGATCTGCCCAGTGAAGAGGAGGA  240
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Qy    301 GAAGTTAAGCCTAAATCAGAGAAGAGAGGGCTCCCTGAAGTTAGGAGGATCTACCTACTCTGTT  360
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Db    301 GAAGTTAAGCCTAAATCAGAGAAGAGAGGGCTCCCTGAAGTTAGGAGGATCTACCTACTCTGTT  360

Qy    361 GAGGCTCCTGGAGATCCTCAAGAGAACCCCAGAAATAAATGCCCACAGGGA  420
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Qy    961 CTGCCCTCTGACTTCAGCCGCCTACTTCCAAATATGAGGGGGTCTCTGACTACACCGGT  1020
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Db    961 CTGCCCTCTGACTTCAGCCGCCTACTTCCAAATATGAGGGGGTCTCTGACTACACCGGT  1020

Qy   1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGTGCTAAGCAGCTC  1080
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Db   1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGTGCTAAGCAGCTC  1080

Qy   1081 CACACCCCTCTCGACACCCTGTGGGGACCTGGTTGACTCTCGGGTTCCGA  1140
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Db   1081 CACACCCCTCTCGACACCCTGTGGGGACCTGGTTGACTCTCGGGTTCCGA  1140

Qy   1141 GCGACGCAGCCTTTGAATGGGCGAGTGAGTTGAGGCCTCCTTCCCGGCTGGAGCAGC  1200
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Db   1201 AGTCCTTCGGGCTCTGACCCAGTCCAGTGAATTCCTCCTGCTGCGCATCCTA  1260

Qy   1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGGCGTTCCTTGTGCAGATGAGA  1320
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Qy   1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTGAGCTACCGGCAGGGTAGCCCGAG  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTGAGCTACCGGCAGGGTAGCCCGAG  1380

Qy   1381 ACTGGAGCCTAGAGGCTGGGATCTTGGAGAATGTGAGAAGCCAGCAGAGGCATCTGAGGG  1440
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Db   1381 ACTGGAGCCTAGAGGCTGGGATCTTGGAGAATGTGAGAAGCCAGCAGAGGCATCTGAGGG  1440

Qy   1441 GGAGCCGGTAACTGTCCTGTCCCAGTTCCTTTTAACTGCCAAGAAATT  1500
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Qy   1501 TTTTAAAATAAAATATTTTATAAT  1522
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Db   1501 TTTTAAAATAAAATATTTTATAAT  1522
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;    OPERATING SYSTEM:  PC-DOS/MS-DOS
;    SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,862B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,504
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/485,862B
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO: 1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1522 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-485-862B-1

Query Match             100.0%;  Score 1522;  DB 2;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy         1 ACAGTCAGCCGCAATGGCTCCCCTGTGCCCCAGCCCTCCCTCTGGTTGATCCCGGCC   60
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Db         1 ACAGTCAGCCGCAATGGCTCCCCTGTGCCCCAGCCCTCCCTCTGGTTGATCCCGGCC   60

Qy        61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTTCGATGCCTGTCCAT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTTCGATGCCTGTCCAT  120

Qy       121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCTTGGGAGGAGCTCTTCTGGGGAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCTTGGGAGGAGCTCTTCTGGGGAA  180

Qy       181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGGAGGAT  240
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Db       181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGGAGGAT  240

Qy       241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT  300

Qy       301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCCTGGGAAGTTAGAGGATCTACCTACTGTT  360
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Db       301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCCTGGGAAGTTAGAGGATCTACCTACTGTT  360

Qy       361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT  420

Qy       421 GACCAGAGTCATTGGCGCTTATGGAGGCGGACCCGGCCTGGCCCGGCCAGCCTGC  480
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Db       421 GACCAGAGTCATTGGCGCTTATGGAGGCGGACCCGGCCTGGCCCGGCCAGCCTGC  480

Qy       481 GCGGGCACGCTTCCAGTCCCCGGTGGGATATCCGCGCGCCGCCCAGCTCGCCGCCGGGC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCGGGCACGCTTCCAGTCCCCGGTGGGATATCCGCGCGCCGCCCAGCTCGCCGCCGGGC  540

Qy       541 CTGCGCCCCCTGGAACTCCTGGGGCTTCCAGCTCCCGGCGCTCCCAGAACTGCGCGCCTGGGC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CTGCGCCCCCTGGAACTCCTGGGGCTTCCAGCTCCCGGCGCTCCCAGAACTGCGCGCCTGGGC  600

Qy       601 AACAATGGGCCACAGTGTGCAAACTGACCCTGCCTCCTTGGGCTTGGGCTTAGAGGATTGGCTCTTGGGGTCC  660
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Db       601 AACAATGGGCCACAGTGTGCAAACTGACCCTGCCTCCTTGGGCTTGGGCTTAGAGGATTGGCTCTTGGGGTCC  660

Qy       661 GGGGCGGGGACGTACCGGGGCTCTTGCACTGCATTCTGACTGACTGGGGGGTTGCGCAGTCGTCCGGGGC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGGGCGGGGACGTACCGGGGCTCTTGCACTGCATTCTGACTGACTGGGGGGTTGCGCAGTCGTCCGGGGC  720

Qy       721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  780

Qy       781 ACCGCCTTTGCCCAGAGTTGACGAGGCCCTTGGGGGTCCGGGGGCGCCCCGGGGAGGCC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ACCGCCTTTGCCCAGAGTTGACGAGGCCCTTGGGGGTCCGGGGGCGCCCCGGGGAGGCC  840

Qy       841 GCCTTTCTCGGAGGAGGAGGGGCCCCGGAAGAAAACAGTGGCCTAGTGAGTTGCTGTTCTCGGCTTG  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCCTTTCTCGGAGGAGGAGGGGCCCCGGAAGAAAACAGTGGCCTAGTGAGTTGCTGTTCTCGGCTTG  900

Qy       901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTGCCCAGGACTGGACATATCTGCACTC  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTGCCCAGGACTGGACATATCTGCACTC  960

Qy       961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTTCTCTGACTACACCGCCCGT  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTTCTCTGACTACACCGCCCGT  1020

Qy      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGACAGTGAGTGCTAAGCAGCTC  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGACAGTGAGTGCTAAGCAGCTC  1080

Qy      1081 CACACCCTCTCTGACACCCGTGGGGGACCCTGGGTGACTCTGGGTACAGCTGAACTTCCGA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CACACCCTCTCTGACACCCGTGGGGGACCCTGGGTGACTCTGGGTACAGCTGAACTTCCGA  1140

Qy      1141 GCGACGCAGCCTTTGAAATGGGCGAGTGATTGATTGGAGGGCCTCCTTCCCTGCTGAGTGGACAGC  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GCGACGCAGCCTTTGAAATGGGCGAGTGATTGATTGGAGGGCCTCCTTCCCTGCTGAGTGGACAGC  1200

Qy      1201 AGTCCTCGGGGCTGCTGCTTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCTGCCTGGCATCCTA  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AGTCCTCGGGGCTGCTGCTTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCTGCCTGGCATCCTA  1260

Qy      1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGCACCAGCGTGCGGTTCCTTGTGCAGATGAGA  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGCACCAGCGTGCGGTTCCTTGTGCAGATGAGA  1320

Qy      1321 AGGCAGCACAGAAGGGGGACCAAAGGGTGTGACCTACCGCCACAGAGGTAGCCGAG  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 AGGCAGCACAGAAGGGGGACCAAAGGGTGTGACCTACCGCCACAGAGGTAGCCGAG  1380

Qy      1381 ACTGGAGCCTTAGAGGCTGGATCTTGGAGAATGTGAGAAGGCCAGAGGCCATCTGAGGG  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 ACTGGAGCCTTAGAGGCTGGATCTTGGAGAATGTGAGAAGGCCAGAGGCCATCTGAGGG  1440

Qy      1441 GGAGGCGGGTAACTGTCCTGCGTCCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAAATT  1500
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Db      1441 GGAGGCGGGTAACTGTCCTGCGTCCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAAATT  1500

Qy      1501 TTTTAAAATAAAATAATTTATAAAT  1522
             |||||||||||||||||||||||||
Db      1501 TTTTAAAATAAAATAATTTATAAAT  1522


RESULT 5
US-08-787-739-1
; Sequence 1, Application US/08787739
; Patent No. 6027887
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
```

```
;  TITLE OF INVENTION:  MN Gene and Protein
;  NUMBER OF SEQUENCES:  96
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  Leona L. Lauder
;  STREET:  369 Pine Street, Suite 610
;  CITY:  San Francisco
;  STATE:  California
;  COUNTRY:  USA
;  ZIP:  94104
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  Floppy disk
;  COMPUTER:  IBM PC compatible
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;  SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER:  US/08/787,739
;  FILING DATE:  24-JAN-1997
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/485,049
;  FILING DATE:  07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/486,756
;  FILING DATE:  07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/477,504
;  FILING DATE:  07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/481,658
;  FILING DATE:  07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/485,862
;  FILING DATE:  07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/485,863
;  FILING DATE:  07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  US 08/487,077
;  FILING DATE:  07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Lauder, Leona L.
;  REGISTRATION NUMBER:  30,863
;  REFERENCE/DOCKET NUMBER:  D-0021.4
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  415-981-2034
;  TELEFAX:  415-981-0332
;  INFORMATION FOR SEQ ID NO:  1:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:  1522 base pairs
;  TYPE:  nucleic acid
;  STRANDEDNESS:  double
;  TOPOLOGY:  linear
;  MOLECULE TYPE:  cDNA
;  HYPOTHETICAL:  NO
;  ANTI-SENSE:  NO
US-08-787-739-1

Query Match         100.0%;  Score 1522;  DB 3;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 ACAGTTCAGCCGCATGGCTCCCCGTGTGCCCCAGCGCCCTCCCCTGTTGAATCCCCGCCGCC    60
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Db       1 ACAGTTCAGCCGCATGGCTCCCCGTGTGCCCCAGCGCCCTCCCCTGTTGAATCCCCGCCGCC    60

Qy      61 CCTGCTCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGAATGCCTGTGTCCAT   120
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Db      61 CCTGCTCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGAATGCCTGTGTCCAT   120

Qy     121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA   180
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Db     121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA   180

Qy     181 GATGACCACTCGGGACGGAGGAGATCTCCCCAGTGAGGAGGAGGATTCACCCAGAGGAGGAGGAT   240
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Db     181 GATGACCACTCGGGACGGAGGAGATCTCCCCAGTGAGGAGGAGGATTCACCCAGAGGAGGAGGAT   240

Qy     241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT   300
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Db     241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT   300

Qy     301 GAAGTTAAGCCTAAAATCAGAAGAAGAGAGGGCTCCCTGAAGTTAGAGGATTACCTGTT   360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GAAGTTAAGCCTAAAATCAGAAGAAGAGAGGGCTCCCTGAAGTTAGAGGATTACCTGTT   360

Qy     361 GAGGCTCCTGGAGATCCTCAAGAACCCACAGCCCCAGAATAAATGCCACAGGACAAAAGAGAGGGGAT   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAGGCTCCTGGAGATCCTCAAGAACCCACAGCCCCAGAATAAATGCCACAGGACAAAAGAGAGGGGAT   420

Qy     421 GACCAGAGTCATTGGGCGTTATGGAGGCGGACACCCGCCCCCCAGCCCCCCCAGCCCTGC   480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GACCAGAGTCATTGGGCGTTATGGAGGCGGACACCCGCCCCCCAGCCCCCCCAGCCCTGC   480

Qy     481 GCGGGGCCGCTTCCAGTCCCGGTGGATATCCGGCCCCCCCCCAGCTGGCCCCTTCGGCCCC   540
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Db     481 GCGGGGCCGCTTCCAGTCCCGGTGGATATCCGGCCCCCCCCCAGCTGGCCCCTTCGGCCCC   540

Qy     541 CTGCGCCCCCTGAAACTCCTGGGCTTTCCAGCTCCCTGGCCCCCTCCCAGAACTGCGCGCCTGCGC   600
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Db     541 CTGCGCCCCCTGAAACTCCTGGGCTTTCCAGCTCCCTGGCCCCCTCCCAGAACTGCGCGCCTGCGC   600

Qy     601 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC   660
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Db     601 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC   660

Qy     661 GGGGCGGGAGGTACCGGGCGTCTGCAGCTCGCATCTGCACTCGGGGGGCTGCAGGTCGTCCGGGGC   720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GGGGCGGGAGGTACCGGGCGTCTGCAGCTCGCATCTGCACTCGGGGGGCTGCAGGTCGTCCGGGGC   720

Qy     721 TCGGAGCACACTGTGGGAAGGGCCACCGTTTCCCTGCCGAGAATCCACGTGGTTCACCTCAGC   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TCGGAGCACACTGTGGGAAGGGCCACCGTTTCCCTGCCGAGAATCCACGTGGTTCACCTCAGC   780

Qy     781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTTGGGGAGGCCTAGAGATGGCTCTGGCC   840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTTGGGGAGGCCTAGAGATGGCTCTGGCC   840

Qy     841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCCTATGAGCAGTTGCCTGCTTG   900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCCTATGAGCAGTTGCCTGCTTG   900

Qy     901 GAAGAAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACATATCCACTC   960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GAAGAAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACATATCCACTC   960

Qy     961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCCCTGT   1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCCCTGT   1020

Qy    1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAATGCTGAGTGGCTAAGCAGCTC   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAATGCTGAGTGGCTAAGCAGCTC   1080

Qy    1081 CACACCCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTGACTGAACTTCGA   1140
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Db    1081 CACACCCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTGACTGAACTTCGA   1140

Qy    1141 GCGACGCAGCCCTTTGAATGGGCGGAGTGAAGGGCCTCCTTCCCTGCTGGAGTGGACAGC   1200
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Db    1141 GCGACGCAGCCCTTTGAATGGGCGGAGTGAAGGGCCTCCTTCCCTGCTGGAGTGGACAGC   1200

Qy    1201 AGTCCTCGGGGCTGCTGAGCCAGTCCAGTCGAATTCCTGCCTGAATTCCTGCCTGAACATCCTA   1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AGTCCTCGGGGCTGCTGAGCCAGTCCAGTCGAATTCCTGCCTGAATTCCTGCCTGAACATCCTA   1260

Qy    1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGGCGTCGGGTTCCTTGTGCAGATGAGA   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGGCGTCGGGTTCCTTGTGCAGATGAGA   1320
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RESULT 6

US-08-487-077A-1

; Sequence 1, Application US/08487077A

; Patent No. 6069242

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia

; APPLICANT: Pastorek, Jaromir

; TITLE OF INVENTION: MN Gene and Protein

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder

; STREET: 6 Mariposa Court

; CITY: Tiburon

; STATE: California

; COUNTRY: USA

; ZIP: 94920

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,077A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-435-2034

; TELEFAX: 415-435-0727

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1522 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-487-077A-1

Query Match   100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity   100.0%;
Matches 1522;   Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1141 GCGACGCAGCCTTTGAATGGGGGAGTGATGATTGAGGCCTCCTTTCCCTGCTGGAGTGGACAGC 1200
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Db   1141 GCGACGCAGCCTTTGAATGGGGGAGTGATGATTGAGGCCTCCTTTCCCTGCTGGAGTGGACAGC 1200

Qy   1201 AGTCCTCCGGGCTGCTGAGCCAGTGCAGCTGAATTCCTGCCTGCTGCTGTCGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCCTCCGGGCTGCTGAGCCAGTGCAGCTGAATTCCTGCCTGCTGCTGTCGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTTGGCCTTCCTTTTTTTTGCTCTTTGTCACCAGGCGTGCCGGTTCCTTGTGTTTCACAGGGAGA 1320
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Db   1261 GCCCTGGTTTTTGGCCTTCCTTTTTTTTGCTCTTTGTCACCAGGCGTGCCGGTTCCTTGTGTTTCACAGGGAGA 1320

Qy   1321 AGGCAGCACAGAAGGAGGGAACCAAAAGGGGGTGTGAGCTACCGGCTGGTTGCAGATGAGA 1380
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Db   1321 AGGCAGCACAGAAGGAGGGAACCAAAAGGGGGTGTGAGCTACCGGCTGGTTGCAGATGAGA 1380

Qy   1381 ACTGGAGGCCTAGGACTGGGATCTTGGAGAAATGTGAGAAGCCACCAGGAGGGCATCTGAGGG 1440
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Db   1381 ACTGGAGGCCTAGGACTGGGATCTTGGAGAAATGTGAGAAGCCACCAGGAGGGCATCTGAGGG 1440

Qy   1441 GGAGCCGGTAACTGTCTCCGTCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCGGTAACTGTCTCCGTCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAATATATTTATAAT 1522
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Db   1501 TTTTAAAATAAATATTTATAAT 1522
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RESULT 7

US-08-485-863A-1

; Sequence 1, Application US/08485863A

Patent No. 6093548

; GENERAL INFORMATION:

　APPLICANT: Zavada, Jan
　APPLICANT: Pastorekova, Silvia
　APPLICANT: Pastorek, Jaromir
　TITLE OF INVENTION: MN Gene and Protein
　NUMBER OF SEQUENCES: 86
　CORRESPONDENCE ADDRESS:
　ADDRESSEE: Leona L. Lauder
　STREET: 6 Mariposa Court
　CITY: Tiburon
　STATE: California
　COUNTRY: USA
　ZIP: 94920
　COMPUTER READABLE FORM:
　MEDIUM TYPE: Floppy disk
　COMPUTER: IBM PC compatible
　OPERATING SYSTEM: PC-DOS/MS-DOS
　SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
　CURRENT APPLICATION DATA:
　APPLICATION NUMBER: US/08/485,863A
　FILING DATE: 07-JUN-1995
　CLASSIFICATION: 514
　PRIOR APPLICATION DATA:
　APPLICATION NUMBER: US 08/260,190
　FILING DATE: 15-JUN-1994
　ATTORNEY/AGENT INFORMATION:
　NAME: Lauder, Leona L.
　REGISTRATION NUMBER: 30,863
　REFERENCE/DOCKET NUMBER: D-0021.3G
　TELECOMMUNICATION INFORMATION:
　TELEPHONE: 415-435-2034
　TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

　LENGTH: 1522 base pairs
　TYPE: nucleic acid
　STRANDEDNESS: single
　TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-485-863A-1

Query Match　100.0%;　Score 1522;　DB 3;　Length 1522;
Best Local Similarity　100.0%;　Pred. No. 0;
Matches 1522;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Qy   1 ACAGTCAGCCGCATGGGCTCCCCTGTGCCCCAGCCCCTGCCCTCTGTTGATCCCGGCC 60
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Db   1 ACAGTCAGCCGCATGGGCTCCCCTGTGCCCCAGCCCCTGCCCTCTGTTGATCCCGGCC 60

Qy  61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTCGTCACTGCCTGTTCCAT 120
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Db  61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTCGTCACTGCCTGTTCCAT 120

Qy 121 CCCCAGAGGTTGCCCGGCGAGGAGAATCCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
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Db 121 CCCCAGAGGTTGCCCGGCGAGGAGAATCCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Qy 181 GATGACCCACTGGGCGCGAGGGATCTGCCCAGTGAAGGAGGAGGAGGAGGAGGAT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GATGACCCACTGGGCGCGAGGGATCTGCCCAGTGAAGGAGGAGGAGGAGGAGGAT 240

Qy 241 CCACCCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CCACCCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 300

Qy 301 GAAGTTAAGCCTAAAATCAGGAAGAAGGAGGCTCCCTGAAGTTAGAGGATTAGAGGATCTACTACTGTT 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GAAGTTAAGCCTAAAATCAGGAAGAAGGAGGCTCCCTGAAGTTAGAGGATTAGAGGATCTACTACTGTT 360

Qy 361 GAGGCTCCTGGAGATCCTCAAGGAACCCCAGAATAAATGCCCACAGGGACAAAAGAAGGGGAT 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GAGGCTCCTGGAGATCCTCAAGGAACCCCAGAATAAATGCCCACAGGGACAAAAGAAGGGGAT 420

Qy 421 GACCAGAGTGCATTGGGCGCTATGGAGGGCACACCCCCTTGGCCCCAGCCTGC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 GACCAGAGTGCATTGGGCGCTATGGAGGGCACACCCCCTTGGCCCCAGCCTGC 480

Qy 481 GCGGGCGGGAGGCTTCCAGTCCCGTGGAATCCGCGCCCCCAGCGTCGCCGCCTTCTCGCCGGCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GCGGGCGGGAGGCTTCCAGTCCCGTGGAATCCGCGCCCCCAGCGTCGCCGCCTTCTCGCCGGCC 540

Qy 541 CTGGCGCCCCCCTGGAAACTCCTGGGCCTTCCAGCTCCCCGGCCGCTCCCCGGCCCTGGGC 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CTGGCGCCCCCCTGGAAACTCCTGGGCCTTCCAGCTCCCCGGCCGCTCCCCGGCCCTGGGC 600

Qy 601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGCCTCTCCGCGGGCTCCTGGGTCCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGCCTCTCCGCGGGCTCCTGGGTCCC 660

Qy 661 GGGCGGGAGGTACCGGGTCTTGGATTATCCGGGCCCCCCAGCTCAGCTCGTCCGGGCAGGTCGTCCGGGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GGGCGGGAGGTACCGGGTCTTGGATTATCCGGGCCCCCCAGCTCAGCTCGTCCGGGCAGGTCGTCCGGGC 720

Qy 721 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGGGTTCACTCAGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 721 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGGGTTCACTCAGC 780

Qy 781 ACCGGCCTTTGCCAGAGGGGCCCGGAAGAAACAGTGCCTTGGGGCGCCCGGAGGCCCGTGGTGCC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 ACCGGCCTTTGCCAGAGGGGCCCGGAAGAAACAGTGCCTTGGGGCGCCCGGAGGCCCGTGGTGCC 840

Qy 841 GCCTTTCTGGAGGAGGAGGCCCGGAAGAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCGCTTG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 GCCTTTCTGGAGGAGGAGGCCCGGAAGAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCGCTTG 900

Qy 901 GAAGAAAATCGCTGAGGAGAGAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 GAAGAAAATCGCTGAGGAGAGAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy 961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGCTCTGACTACACGCCCCTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGCTCTGACTACACGCCCCTGT 1020
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RESULT 8
US-08-485-049D-1
; Sequence 1, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-049D-1

Query Match   100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity   100.0%;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

[sequence alignment data]

RESULT 9
US-09-178-115-1
; Sequence 1, Application US/0917811S
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; FILE REFERENCE: D-0021.5A
; TITLE OF INVENTION: MN Gene and Protein
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY:
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)

US-09-178-115-1

Query Match   100.0%;   Score 1522;   DB 3;   Length 1522;
Best Local Similarity   100.0%;
Matches 1522;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 ACAGTTCAGCCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCTCTGTTGATCCCGGCC   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTTCAGCCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCTCTGTTGATCCCGGCC   60

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTTCTTCACTGCTTCTGAATGCCTCCAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTTCTTCACTGCTTCTGAATGCCTCCAT  120

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGA  180

Qy    181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAACAGAGGATTCACCCAGAGAGGAGGAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAACAGAGGATTCACCCAGAGAGGAGGAT  240

Qy    241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACT  300

Qy    301 GAAGTTAAGCCTAAATCAGAAGAGAGAGAGGGGCTCCCTGAAGTTAGAGCTTACCTACTGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAAGTTAAGCCTAAATCAGAAGAGAGAGAGGGGCTCCCTGAAGTTAGAGCTTACCTACTGTT  360

Qy    361 GAGGCTCCTGGGACATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGGAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGGACATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT  420

Qy    421 GACCAGAGTCATTGGCGCGCTATGGGAGGCGGACCCCGCCCCTGGCGTCCCCAGCCTGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GACCAGAGTCATTGGCGCGCTATGGAGGCGGACCCCGCCCCTGGCGTCCCCAGCCTGC  480

Qy    481 GCGGGGCGCCGCTTCCAGTCCCCGGTGGAATATCCGGCCGCCTTCTGCCCCGGCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGGCGCCGCTTCCAGTCCCCGGTGGATATCCGGCCGCCTTCTGCCCCGGCC  540

Qy    541 CTGCGCCCCTGGAACTCCTGGCTTCCAGCTCCCAGCTCCCAGAACTGCCCTGCGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGCGCCCCTGGAACTCCTGGCTTCCAGCTCCCAGCTCCCAGAACTGCCCTGCGC  600

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCTCGGGCCTAGAGATGGCTCTGGGTCCC  660
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Qy   841 GCCCTTCTCGGAGGAGGGCCCGGAGGAGAAACAGTGCCTATGAGCAGTTGCTGTCGGCTTG   900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCCCTTCTCGGAGGAGGGCCCGGAGGAGAAACAGTGCCTATGAGCAGTTGCTGTCGGCTTG   900

Qy   901 GAAGAAATCGCTGAGGAGAGGCTCAGAGACTCAGGTCACGTCTC   960
        ||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAAGAAATCGCTGAGGAGAGGCTCAGAGACTCAGGTCACGTCTC   960

Qy   961 CTGCCCTCTGACTTCAGCCGCGCTACTTCCAATATGAGAGGGGTCTCTCTGGACTACACCACCGCCCCTGT   1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CTGCCCTCTGACTTCAGCCGCGCTACTTCCAATATGAGAGGGGTCTCTCTGGACTACACCACCGCCCCTGT   1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAGTGATGCTGAGTGCTAAGCAGCTC   1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAGTGATGCTGAGTGCTAAGCAGCTC   1080

Qy   1081 CACACCCCTCTGACACCCTGTGGGGACCTGGTCACTCTCGGCTACACGTGAACTTCCGA   1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCCTCTGACACCCTGTGGGGACCTGGTCACTCTCGGCTACACGTGAACTTCCGA   1140

Qy   1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGGCGTCCCAGGCCTCCTTCCCTGCTGGAGTGGGACAGC   1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGGCGTCCCAGGCCTCCTTCCCTGCTGGAGTGGGACAGC   1200

Qy   1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGCGCTGCTGGTGACATCCTA   1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGCGCTGCTGGTGACATCCTA   1260

Qy   1261 GCCCTGGTTTTTGGCCCTCCTTTTTGCTGTCGTTCCTTGTGCAGATGAGA   1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCTGGTTTTTGGCCCTCCTTTTTGCTGTCGTTCCTTGTGCAGATGAGA   1320

Qy   1321 AGGCAGCACAGAGAGGGGGAACCAAAGGGGGAGGGTGTGAGCTGAGCCGAGAGTGAGCCGAG   1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGCAGCACAGAGAGGGGGAACCAAAGGGGGAGGGTGTGAGCTGAGCCGAGAGTGAGCCGAG   1380

Qy   1381 ACTGGGAGGCCTAGAGGCTGGATCTTGGACAAATGTGAGAAGCCAGCCAGCAGCATCTGAGG   1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACTGGGAGGCCTAGAGGCTGGATCTTGGACAAATGTGAGAAGCCAGCCAGCAGCATCTGAGG   1440

Qy   1441 GGAGCCCGGTAACTGTCCTGCTGCTCATTATGCCCACTTCCTTTTAACTGCCAAGAAATT   1500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCCGGTAACTGTCCTGCTGCTCATTATGCCCACTTCCTTTTAACTGCCAAGAAATT   1500

Qy   1501 TTTTAAAATAAATATATTTATAAT   1522
        ||||||||||||||||||||||||
Db   1501 TTTTAAAATAAATATATTTATAAT   1522

RESULT 10
US-09-177-776-1
; Sequence 1, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein

; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
;
SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY:
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-09-177-776-1

Query Match   100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[Sequence alignment data — Qy (query) and Db (database) rows with residue position numbering from 1 to 1522, dense DNA sequence with alignment bars]

RESULT 11
US-09-772-719B-1
; Sequence 1, Application US/09772719B
; Patent No. 6770438
GENERAL INFORMATION:
  APPLICANT:
    Zavada, Jan
    Pastorekova, Silvia
    Pastorek, Jaromir
  TITLE OF INVENTION: MN Gene and Protein
  NUMBER OF SEQUENCES: 86
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Leona L. Lauder
    STREET: 465 California Street, Suite 450
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94104
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/772,719B
    FILING DATE: 30-Jan-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/485,049
    FILING DATE: 07-JUN-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Lauder, Leona L.
    REGISTRATION NUMBER: 30,863
    REFERENCE/DOCKET NUMBER: D-0021.3A-2
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-981-2034
    TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1522 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-772-719B-1

Query Match   100.0%;   Score 1522;   DB 4;   Length 1522;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

(Sequence alignment — Query (Qy) / Database (Db) rows, positions 1–1522)

Qy 1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCAGCCCTGCCCCTCGTTGATCCCGGCC 60
Db 1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCAGCCCTGCCCCTCGTTGATCCCGGCC 60

Qy 61 CCTGCTCCAGGCCTCACTGTGCGAACTGCTCGTGCTGTTCACTGTGCTGTTCCAT 120
Db 61 CCTGCTCCAGGCCTCACTGTGCGAACTGCTCGTGCTGTTCACTGTGCTGTTCCAT 120

Qy 121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGGGAGGGCTCTCTTCGGGGAA 180
Db 121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGGGAGGGCTCTCTTCGGGGAA 180

Qy 181 GATGACCCACTGGGCGCGAGGAGGAGGATCTCCCCAGTGAACAGAGGAGGATCTACCT 240
Db 181 GATGACCCACTGGGCGCGAGGAGGAGGATCTCCCCAGTGAACAGAGGAGGATCTACCT 240

Qy 241 CCACCCGGAGGAGGAGGGATCTACCTGGAGGAGGAGGAGGATCTACCT 300

RESULT 12
US-08-260-190-5
; Sequence 5, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 5
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-08-260-190-5

Query Match   100.0%; Score 1522; DB 4; Length 1522;
Best Local Similarity   100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1441 GGAGCCGGTAACGTCCGTCCTGCTCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCGGTAACGTCCGTCCTGCTCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAAATATTTTATTAAT 1522
           |||||||||||||||||||||||||
Db   1501 TTTTAAAATAAAATATTTTATTAAT 1522

RESULT 13
US-08-335-469-1
; Sequence 1, Application US/08335469A
; Patent No. 6004535
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide
; TITLE OF INVENTION: Using MN-Specific Antibodies
; FILE REFERENCE: D-0021A
; CURRENT APPLICATION NUMBER: US/08/335,469A
; CURRENT FILING DATE: 1994-11-07
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-335-469-1

Query Match 91.9%; Score 1399; DB 3; Length 1399;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
Matches 1399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   124 CAGAGGTTGCCCCGGATGCAGAGGAATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAAGAT 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CAGAGGTTGCCCCGGATGCAGAGGAATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAAGAT 60

Qy   184 GACCCACTGGGCCGGAGGAGGATCTGCCCAGTGAAGAGGAATTCACCCAGGAGGAGGATCCA 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GACCCACTGGGCCGGAGGAGGATCTGCCCAGTGAAGAGGAATTCACCCAGGAGGAGGATCCA 120

Qy   244 CCCGGAGAGGAGGATCTACCCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAA 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCGGAGAGGAGGATCTACCCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAA 180

Qy   304 GTTAAGCCTAAATCAGAGAAGAAGAAGGGGGTCCCTGAAGTTAGAGGATCTACCTACTGTTGAG 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTTAAGCCTAAATCAGAGAAGAAGAAGGGGGTCCCTGAAGTTAGAGGATCTACCTACTGTTGAG 240

Qy   364 GCTCCCTGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAAGAAGGGGATGAC 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCTCCCTGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAAGAAGGGGATGAC 300

Qy   424 CAGAGTCATTGCGCTATGGAGGCGACACCGGCCCCTGCCCCGGTGTCCCCAGCCTGCGG 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAGAGTCATTGCGCTATGGAGGCGACACCGGCCCCTGCCCCGGTGTCCCCAGCCTGCGG 360

Qy   484 GCCGCGCTTCCAGTCCCGGTGGATATCCGCGCCCCAGCGTCGCGGCCCTTCGCGCCCTG 543
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; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-260-190-1

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;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      COMPUTER: IBM PC compatible
;      MEDIUM TYPE: Floppy disk
;      COMPUTER READABLE FORM:
;        ZIP: 94105
;        STATE: CA
;        COUNTRY: USA
;        CITY: San Francisco
;        STREET: Plaza
;        STREET: Steuart Street Tower, 18th Fl., One Market
;        ADDRESSEE: Leona L. Lauder
;      CORRESPONDENCE ADDRESS:
;      NUMBER OF SEQUENCES: 4
;      TITLE OF INVENTION: MN Gene and Protein
;        APPLICANT: Pastorek, Jaromir
;        APPLICANT: Pastorekova, Silvia
;        APPLICANT: Zavada, Jan
;      APPLICANT:
;    GENERAL INFORMATION:
;    Patent No. 5387676
;    US-07-964-589-1
;  Sequence 1, Application US/07964589
RESULT 15
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;                                                                       CLASSIFICATION: 435
;                                                                     ATTORNEY/AGENT INFORMATION:
;                                                                       NAME: Lauder, Leona L
;                                                                       REGISTRATION NUMBER: 30,863
;                                                                       REFERENCE/DOCKET NUMBER: D-0021
;                                                                     TELECOMMUNICATION INFORMATION:
;                                                                       TELEPHONE: 415-777-9257
;                                                                       TELEFAX: 415-543-4219
;                                                                     INFORMATION FOR SEQ ID NO: 1:
;                                                                     SEQUENCE CHARACTERISTICS:
;                                                                       LENGTH: 1397 base pairs
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;                                                                       STRANDEDNESS: single
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; US-07-964-589-1

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	1522	100.0	1522	18	US-10-795-933-5	Sequence 5, Appli
4	1522	100.0	1522	16	US-10-888-694-1	Sequence 1, Appli
5	1522	100.0	1552	9	US-09-954-456-89	Sequence 89, Appl
6	1522	100.0	1552	9	US-09-954-456-726	Sequence 726, Appl
7	1522	100.0	1552	10	US-09-960-706-1080	Sequence 1080, Ap
8	1522	100.0	1552	10	US-09-873-367C-516	Sequence 516, App
9	1522	100.0	1552	11	US-09-968-007A-213	Sequence 213, Appl
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11	1522	100.0	1552	15	US-10-465-572-9	Sequence 9, Appli
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ALIGNMENTS

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US-09-772-719-1
Sequence 1, Application US/09772719
Patent No. US20020137910A1

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GENERAL INFORMATION:
   APPLICANT: Zavada, Jan
   APPLICANT: Pastorekova, Silvia
   APPLICANT: Pastorek, Jaromir
   TITLE OF INVENTION: MN Gene and Protein
   NUMBER OF SEQUENCES:  86
   CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Leona L. Lauder
      STREET:  369 Pine Street
      CITY:  San Francisco
      STATE:  California
      COUNTRY:  USA
      ZIP:  94104
   COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
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      APPLICATION NUMBER:  US/09/772,719
      FILING DATE:  30-JAN-2001
      CLASSIFICATION:
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  US 08/485,049
      FILING DATE:  07-JUN-1995
      APPLICATION NUMBER:  US 08/260,190
      FILING DATE:  15-JUN-1994
   ATTORNEY/AGENT INFORMATION:
      NAME:  Lauder, Leona L.
      REGISTRATION NUMBER:  30,863
      REFERENCE/DOCKET NUMBER:  D-0021.3E
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;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-981-2034
;     TELEFAX: 415-981-0332
;  INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH: 1522 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
US-09-772-719-1

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          ||||||||||||||||||||||||||||||||||||||||||
Db    301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTA  360

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCA  420
          |||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCA  420

Qy    421 GACCAGAGTCATTGGCGGCTATGGAGAGGGCGACCCC  480
          |||||||||||||||||||||||||||||||||||||
Db    421 GACCAGAGTCATTGGCGGCTATGGAGAGGGCGACCCC  480

Qy    481 GCGGGGGCCGCTTCCAGTCCCGGTGGATATCCGCGCC  540
          |||||||||||||||||||||||||||||||||||||
Db    481 GCGGGGGCCGCTTCCAGTCCCGGTGGATATCCGCGCC  540

Qy    541 CTGCGCGCCCCCTGGAACTCCTGGGCGCTTCCAGCTCC  600
          ||||||||||||||||||||||||||||||||||||||
Db    541 CTGCGCGCCCCCTGGAACTCCTGGGCGCTTCCAGCTCC  600

Qy    601 AACAATGGCCCACAGTGTGCAACTGACCCTGCCTGCTCC  660
          |||||||||||||||||||||||||||||||||||||||
Db    601 AACAATGGCCCACAGTGTGCAACTGACCCTGCCTGCTCC  660

Qy    661 GGGCCGGGAGTACCGGGCTCTGCAGCTGCATCCACTGCAC  720
          ||||||||||||||||||||||||||||||||||||||||
Db    661 GGGCCGGGAGTACCGGGCTCTGCAGCTGCATCCACTGCAC  720

Qy    721 TCGGAGCACACTGTGGAAGGGCACCGTTTCCCTGCCCAGA  780
          ||||||||||||||||||||||||||||||||||||||||
Db    721 TCGGAGCACACTGTGGAAGGGCACCGTTTCCCTGCCCAGA  780

Qy    781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGCGGCGGG  840
          ||||||||||||||||||||||||||||||||||||||
Db    781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGCGGCGGG  840

Qy    841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGA  900
          ||||||||||||||||||||||||||||||||||||||||||
Db    841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGA  900

Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGA  960
          ||||||||||||||||||||||||||||||||||||||||||
Db    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGA  960

Qy    961 CTGCCCTCCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGT  1020
          |||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGCCCTCCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGT  1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATG  1080
          |||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATG  1080

Qy   1081 CACACCCCTCTCTGACACACCCTGTGGGGGACCTGGTGAC  1140
          ||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCCTCTCTGACACACCCTGTGGGGGACCTGGTGAC  1140

Qy   1141 GCGACGCAGCCTTTGAATGGGCGGAGTGATTGAGGGCTCC  1200
          ||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCTTTGAATGGGCGGAGTGATTGAGGGCTCC  1200

Qy   1201 AGTCCTCCGGGCTCCTGACCCAGTCCAGCTGAATTCCTCC  1260
          ||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCCTCCGGGCTCCTGACCCAGTCCAGCTGAATTCCTCC  1260

Qy   1261 GCCCTGGTTTTTGGCCTCCTTTTGTCGTCACCAGCGTCGC  1320
          ||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCTGGTTTTTGGCCTCCTTTTGTCGTCACCAGCGTCGC  1320

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCG  1380
          |||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCG  1380

Qy   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCA  1440
          ||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCA  1440

Qy   1441 GGAGCCGGTAACTGTCCTGTCCACTTCCTTTTTAACTGCCA  1500
          |||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCGGTAACTGTCCTGTCCACTTCCTTTTTAACTGCCA  1500

Qy   1501 TTTTAAAATAAATAATTATTTTATAAT  1522
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Db   1501 TTTTAAAATAAATAATTATTTTATAAT  1522
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; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-09-967-237-1

Query Match       100.0%;  Score 1522;  DB 10;  Length 1522;
Best Local Similarity  100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
Pred. No. 0;

Qy      1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCTGCTACTTTGGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCTGCTACTTTGGATCCCGGCC 60
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(... sequence alignment blocks 61 through 1522 ...)

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Query Match             100.0%;    Score 1522;    DB 18;    Length 1522;
Best Local Similarity   100.0%;    Pred. No. 0;   Mismatches  0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 ACAGTCAGCCGCAATGGCTCCCCCTTGTCCCCAGCCCCCTGGCTCCTCGTTGCTGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCCGCAATGGCTCCCCCTTGTCCCCAGCCCCCTGGCTCCTCGTTGCTGTTGATCCCGGCC 60

Qy     61 CCTGCTCCAGGGCCTCACTGTGCAACTGCCTGCTGCGTCCCCAGCCCCTGCTCCTGCTTCTGAGTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCTCCAGGGCCTCACTGTGCAACTGCCTGCTGCGTCCCCAGCCCCTGCTCCTGCTTCTGAGTCCAT 120

Qy    121 CCCCAGGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Qy    181 GATGAACCCCACTGCGGCGGAGGAGACTCTGCCCAGTGAAAGAGGAGGATTCACCCAGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGAACCCCACTGCGGCGGAGGAGACTCTGCCCAGTGAAAGAGGAGGATTCACCCAGAGGAGGAT 240

Qy    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTTACCTGGAGGAGGAGGATCTACCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTTACCTGGAGGAGGAGGATCTACCT 300

Qy    301 GAAGTTAAGCCTAAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAAGTTAAGCCTAAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Qy    361 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGGGACAAAGAAAGGGGAT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAAGGGGAT 420

Qy    421 GACCAGAGTCATTGGGCGCTATTGGAGGCGACCCCGCCCCCGGGGGTGTCCCCCAGCCTGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GACCAGAGTCATTGGGCGCTATTGGAGGCGACCCCGCCCCCGGGGGTGTCCCCCAGCCTGC 480

Qy    481 GCGGGGCCGCTTCCAGTCCCCGGTGGATATTCCGGCCCCTTCTGCCCCCGGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGGCCGCTTCCAGTCCCCGGTGGATATTCCGGCCCCTTCTGCCCCCGGCC 540

Qy    541 CTCGCGCCCCCTGGAACTCCTCGGGCTTCCAGCTCCCGCGCCTCCCGAACTGCGCCTGCGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTCGCGCCCCCTGGAACTCCTCGGGCTTCCAGCTCCCGCGCCTCCCGAACTGCGCCTGCGC 600

Qy    601 AACAATGGCCACAGTGTGCAACTGACACCCGCCCTCCTCGGCTGCCTCTCCTGGGTCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACAATGGCCACAGTGTGCAACTGACACCCGCCCTCCTCGGCTGCCTCTCCTGGGTCC 660

Qy    661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCGCATCTGGGGGGGCTGCGGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCGCATCTGGGGGGGCTGCGGC 720

Qy    721 TCGGAGCACACTGTGGAGAGGCCACACGGTTTCCCTGCCGAGATCCACGTCGGTTCACCTCAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TCGGAGCACACTGTGGAGAGGCCACACGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780

Qy    781 ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCGCCGGGGAGGCCCTGGCCGT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCGCCGGGGAGGCCCTGGCCGT 840

Qy    841 GCCTTTCTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGGCTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCCTTTCTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGGCTTG 900

Qy    901 GAAGAAATCGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGACTGGACATAT CTGCACTC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy    961 CTGCCCCTCGACTTCAGCGCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACACCGCCCTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGCCCCTCGACTTCAGCGCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACACCGCCCTGT 1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTAACCAGACAGCAGTGAGTGCTGAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGGTGTCATCTGGACTGTGTTAACCAGACAGCAGTGAGTGCTGAGTGCTAAGCAGCTC 1080

Qy   1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTGCTCGTCGGGTACAGCTTCCGA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTGCTCGTCGGGTACAGCTTCCGA 1140

Qy   1141 GCGACGCAGCCCTTTGAAGTGGGACGCAGTGATTGAGGCCTCCTTCCCTGTTCCCTTGCTTCTTGGAGTGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCCTTTGAAGTGGGACGCAGTGATTGAGGCCTCCTTCCCTGTTCCCTTGCTTCTTGGAGTGGACAGC 1200

Qy   1201 AGTCCTCGGGCTGCTGAGGCCAGTCCAGCTGAATTCCTGCCTGCTGGCTGCGTGGGTTGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCCTCGGGCTGCTGAGGCCAGTCCAGCTGAATTCCTGCCTGCTGGCTGCGTGGGTTGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTGGCCCTCCTTTTTGCTGTCACCAGCGTCGCGGTTCCTTGTTGCAGATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCTGGTTTTGGCCCTCCTTTTTGCTGTCACCAGCGTCGCGGTTCCTTGTTGCAGATGAGA 1320

Qy   1321 AGGCAGCACAGAGAGGGAACCAAAGGGGGTGTGAGGCTACCGCCCAGCACAGAGTAGCCGAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGCAGCACAGAGAGGGAACCAAAGGGGGTGTGAGGCTACCGCCCAGCACAGAGTAGCCGAG 1380

Qy   1381 ACTGGAGCCTAGAGGGCTGGATCTTGGAGAAGTTGGAGAAGCAGCCAGAGGCATCTGAGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACTGGAGCCTAGAGGGCTGGATCTTGGAGAAGTTGGAGAAGCAGCCAGAGGCAATCTGAGGG 1440

Qy   1441 GGAGCCGGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAAGTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCGGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAAGTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAAATATTTTATAAT 1522
          ||||||||||||||||||||||||
Db   1501 TTTTAAAATAAAATATTTTATAAT 1522
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;   TELEPHONE: 415-981-2034
;   TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1522 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-888-694-1

Query Match       100.0%;  Score 1522;  DB 18;  Length 1522;
Best Local Similarity  100.0%;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      1 ACAGTTCAGCCGCCGACATGGCTCCCTGTGTCCCCTGTTGCCCCAGCGCCCTCCCTCTCTGTTGATCCCGGCC  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTTCAGCCGCCGACATGGCTCCCTGTGTCCCCTGTTGCCCCAGCGCCCTCCCTCTCTGTTGATCCCGGCC  60

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT  120

Qy    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGAGGAA  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGAGGAA  180

Qy    181 GATGACCCACTCGGCGAGGAGGATCTGCCCAGTGAAGACGAGGAGGAT  240
Db    181 GATGACCCACTCGGCGAGGAGGATCTGCCCAGTGAAGACGAGGAGGAT  240

Qy    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGATCTACCT  300
Db    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGATCTACCT  300

Qy    301 GAAGTTAAGCCTAAATCAGAAGAAGAGGAGGATCTACCCAGTGAAGTTAGAGGATCTACCTACTGTT  360
Db    301 GAAGTTAAGCCTAAATCAGAAGAAGAGGAGGATCTACCCAGTGAAGTTAGAGGATCTACCTACTGTT  360

Qy    361 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT  420
Db    361 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT  420

Qy    421 GACCAGAGTCATTGGGCGTATGGAGGCGACCCGGCCCTGCCCGGTGTCCCCAGCCTGC  480
Db    421 GACCAGAGTCATTGGGCGTATGGAGGCGACCCGGCCCTGCCCGGTGTCCCCAGCCTGC  480

Qy    481 GCGGGCCGCGCTTCCAGTCCCGGTTGGATAATCCGGCGCGCTTCTGCCCGGCC  540
Db    481 GCGGGCCGCGCTTCCAGTCCCGGTTGGATAATCCGGCGCGCTTCTGCCCGGCC  540

Qy    541 CTGCGCCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGGCTCCCCAGAACTGCGCCTGCGC  600
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Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTCCTGGGCTAGAGATGGCTCTGGGTCCC  660
Db    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTCCTGGGCTAGAGATGGCTCTGGGTCCC  660

Qy    661 GGGCGGGGAGTACCGGGCTCTGCGACTGCATCTGCAGGTCGTCCGGGC  720
Db    661 GGGCGGGGAGTACCGGGCTCTGCGACTGCATCTGCAGGTCGTCCGGGC  720

Qy    721 TCGGAGCACACTGTGGAAGGCACCACGTGTTCACCTCAGC  780
Db    721 TCGGAGCACACTGTGGAAGGCACCACGTGTTCACCTCAGC  780

Qy    781 ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCCGGGGC  840
Db    781 ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCCGGGGC  840
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Qy    841 GCCTTTCTCGGAGGAGGGGCCCGGAAGAAACAGTCCTATGAGCAGTCTTGCTGTCTCGGCTTG  900
Db    841 GCCTTTCTCGGAGGAGGGGCCCGGAAGAAACAGTCCTATGAGCAGTCTTGCTGTCTCGGCTTG  900

Qy    901 GAAGAAATCGCTGAGGAAGGCCTCAGACTCAGGTCCCAGGACTGGGACAGTTGCTGCTCACTC  960
Db    901 GAAGAAATCGCTGAGGAAGGCCTCAGACTCAGGTCCCAGGACTGGGACAGTTGCTGCTCACTC  960

Qy    961 CTGCCCTTCTGACTTCAGCCGCGCCTACTTCCAATATGAGGGGTTCTGACTACACCGCCCTGT  1020
Db    961 CTGCCCTTCTGACTTCAGCCGCGCCTACTTCCAATATGAGGGGTTCTGACTACACCGCCCTGT  1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGCAGTGATGCTGAGTGCTGTGTCTCTCGGCTC  1080
Db   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGCAGTGATGCTGAGTGCTGTAAGGCAGCTC  1080

Qy   1081 CACACCCTTCTGACACCCGTGTGGGCAACCTGGTGACTCTCGGGCTTACAGCTGAACTTCCGA  1140
Db   1081 CACACCCTTCTGACACCCGTGTGGGCAACCTGGTGACTCTCGGGCTTACAGCTGAACTTCCGA  1140

Qy   1141 GCGACGCAGCCTTTGAAATGGGCGGAGTGAGTGATTGATTGAGTGAGCAGC  1200
Db   1141 GCGACGCAGCCTTTGAAATGGGCGGAGTGAGTGATTGATTGAGTGAGCAGC  1200

Qy   1201 AGTCCTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCTGCTGCTGTCGTGGTGACATCCTA  1260
Db   1201 AGTCCTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCTGCTGCTGTCGTGGTGACATCCTA  1260

Qy   1261 GCCCTGGTTTTTGGGCCTCCTTTTCTGCTACCAGCGTCGGCGGTTCCTTGTGCAGATGAGA  1320
Db   1261 GCCCTGGTTTTTGGGCCTCCTTTTCTGCTACCAGCGTCGGCGGTTCCTTGTGCAGATGAGA  1320

Qy   1321 AGGCAGCACAGAGGGGACCAAAAGGGAGGTGTGAGCTACCGCGCCAGCAGAGGTAGCCGAG  1380
Db   1321 AGGCAGCACAGAGGGGACCAAAAGGGAGGTGTGAGCTACCGCGCCAGCAGAGGTAGCCGAG  1380

Qy   1381 ACTGGAGCCTAGAGGCTGGAATGTGAGAAGCCAGCAGGCCATCTGAGGG  1440
Db   1381 ACTGGAGCCTAGAGGCTGGAATGTGAGAAGCCAGCAGGCCATCTGAGGG  1440

Qy   1441 GGAGCCGGGTAACTGTCCTCGTGTCCGTTCATTATGCCACTTCCTTTTAAACTGCCAAGAAATT  1500
Db   1441 GGAGCCGGGTAACTGTCCTCGTGTCCGTTCATTATGCCACTTCCTTTTAAACTGCCAAGAAATT  1500

Qy   1501 TTTTAAAATAAATATTTTATAAT  1522
Db   1501 TTTTAAAATAAATATTTTATAAT  1522
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RESULT 5
US-09-954-456-89
; Sequence 89, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26

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;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: Patentin version 3.0
;
;  SEQ ID NO 89
;  LENGTH: 1552
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-954-456-89

Query Match           100.0%;  Score 1522;  DB 9;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ACAGTCAGCCGCAATGGCTCCCCTGTGCCCCTGGCTCCCTCCCTCTGTTGATCCCCGGCC 60
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Db      1 ACAGTCAGCCGCAATGGCTCCCCTGTGCCCCTGGCTCCCTCCCTCTGTTGATCCCCGGCC 60
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;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: Patentin version 3.0
;
;  SEQ ID NO 726
;  LENGTH: 1552
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-954-456-726

Query Match        100.0%;  Score 1522;  DB 9;  Length 1552;
Best Local Similarity  100.0%;  Pred. No. 0;  Mismatches 0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        1 ACAGTCAGCGCGCAATGGCTCCCCGTCTCCCCTGCCCCCAGCCCCTGGCTCTCGTTGATCCCGGCC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       31 ACAGTCAGCGCGCAATGGCTCCCCGTCTCCCCTGCCCCCAGCCCCTGGCTCTCGTTGATCCCGGCC 90

Qy       61 CCTGCTCTCAGGCCGCCTCACTGTGCTGCTGTCTGTCATGCCTGTGATCCCGGCC 120
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Db       91 CCTGCTCTCAGGCCTTCACTGTGCTGCTGTCTGTCATGCCTGTGATCCCGGCC 150
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[sequence alignment continues through position 1552]

RESULT 7
US-09-960-706-1080
; Sequence 1080, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 1080
; LENGTH: 1552

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080

Query Match          100.0%;  Score 1522;  DB 10;  Length 1552;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ACAGTCAGCCGCATGGCTCTCCCCTGTCCCCAGCCCCTGCCCCAGCCCCTGTTGATCCCGGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTCAGCCGCATGGCTCTCCCCTGTCCCCAGCCCCTGCCCCAGCCCCTGTTGATCCCGGCC 90

Qy     61 CCTGCTTCCAGGCGCTTCACTGTCGCAACTGCTGCTTCTGCTTCGTGATGCCTGTTCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTTCCAGGCGCTTCACTGTCGCAACTGCTGCTTCTGCTTCGTGATGCCTGTTCAT 150

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTTCTGTGGGGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTTCTGTGGGGAA 210

Qy    181 GATGACCCCACTGGGCGGCGAGGAGGATCTGCCCAGTGAAAGGAGGATCACCCAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCCACTGGGCGGCGAGGAGGATCTGCCCAGTGAAAGGAGGATCACCCAGAGGAGGAT 270

Qy    241 CCACCCGGAGAGGAGGATCTACCTGGACGAGGAGGAGGATCTACCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCGGAGAGGAGGATCTACCTGGACGAGGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAAATCAGAGAGAGAAGAGGAGGGCTCCCGGAGAGGAAGTTAGAGGATCTACCTACTGTT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAAATCAGAGAGAGAAGAGGAGGGCTCCCGGAGAGGAAGTTAGAGGATCTACCTACTGTT 390

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGACAAAAGAAGGGGAT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGACAAAAGAAGGGGAT 450

Qy    421 GACCAGAGTCATTGGGCGCTATGTGAGGGCGACCCGCCGCCCCGGGGGTGTCCCCAGCCTGC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 GACCAGAGTCATTGGGCGCTATGTGAGGGCGACCCGCCGCCCCGGGGGTGTCCCCAGCCTGC 510

Qy    481 GCGGGCCCGCCTTCCAGTCCCGGTGGAATATCCGCCCCCAGCTCGGCCTTCGCCCCGGCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GCGGGCCCGCCTTCCAGTCCCGGTGGAATATCCGCCCCCAGCTCGGCCTTCGCCCCGGCC 570

Qy    541 CTGCGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCACGCTCCGCGCGGGCCCTGCGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 CTGCGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCACGCTCCGCGCGGGCCCTGCGC 630

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCCTAGAGATGGGTCCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCCTAGAGATGGGTCCC 690

Qy    661 GGGCGGCGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGTGAGGTCGTCCGGGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 GGGCGGCGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGTGAGGTCGTCCGGGC 750

Qy    721 TCGGGAGCACACTGTTGGAAGGCCACCGTTTCCCTGCCGAGATCCAACGTGGTCACCTCAGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCGGGAGCACACTGTTGGAAGGCCACCGTTTCCCTGCCGAGATCCAACGTGGTCACCTCAGC 810

Qy    781 ACCGCCCTTTGCCAGAGTTGACAGAGGCCTTGGGCGCGCCCGGGGAGGCCCTGGCCGTTGTTGGCC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ACCGCCCTTTGCCAGAGTTGACAGAGGCCTTGGGCGCGCCCGGGGAGGCCCTGGCCGTTGTTGGCC 870

Qy    841 GCCTTTCTCTGGAGGAGGGGCCGGAAGAAAACAGTGCCTTATGAGGCAGTTGCTGCTCGCTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTCTCTGGAGGAGGGGCCGGAAGAAAACAGTGCCTTATGAGGACATATCTGCTCGCTTG 930

Qy    901 GAAGAAATCGCTGAGGAGGAGGCTCAGGACTCAGGTTCCCAGGACTGAGGACATATCTGCACTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 GAAGAAATCGCTGAGGAGGAGGCTCAGGACTCAGGTTCCCAGGACTGAGGACATATCTGCACTC 990

Qy    961 CTGCCCCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACCCCCTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGCCCCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACCCCCTGT 1050

Qy   1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACAGTGAATGCTGAGTGCTTCCGA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACAGTGAATGCTGAGTGCTTCCGA 1110

Qy   1081 CACACCCTTCTCGACAACCCTGTGGGGGACCTGGTGACTCTCGGCGTACAGCTGAACTTCCGA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 CACACCCTTCTCGACAACCCTGTGGGGGACCTGGTGACTCTCGGCGTACAGCTGAACTTCCGA 1170

Qy   1141 GCGACGCAGCCCTTTGAATGGGGCCAGTGATGACTGGGTGAACAGCAGTGGAGTGCTGGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 GCGACGCAGCCCTTTGAATGGGGCCAGTGATGACTGGGTGAACAGCAGTGGAGTGCTGGGACAGC 1230

Qy   1201 AGTCCTCCGGGCTGCCTGAGCCAGTCCAGCTGAATTCCCTGCCGTCTGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 AGTCCTCCGGGCTGCCTGAGCCAGTCCAGCTGAATTCCCTGCCGTCTGGTGACATCCTA 1290

Qy   1261 GCCCTGGTTTTTGGCCTCCTCCTTTTGGCTGTCACCGAGCGTCGGGTTCCTTGTTGCAGATGAGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 GCCCTGGTTTTTGGCCTCCTCCTTTTGGCTGTCACCGAGCGTCGGGTTCCTTGTTGCAGATGAGA 1350

Qy   1321 AGGCAGCACAGGAAGGGGGAACCAAAAGGGGGTGTGAGCGTACCGCCCAGCAGAGGGTAGCCGAG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AGGCAGCACAGGAAGGGGGAACCAAAAGGGGGTGTGAGCGTACCGCCCAGCAGAGGGTAGCCGAG 1410

Qy   1381 ACTGGAGCCTAGAGGCTGGATCTTCTTGGCAAATGTCAGAAGCCAGAGGCCATCTGAGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ACTGGAGCCTAGAGGCTGGATCTTCTTGGCAAATGTCAGAAGCCAGAGGCCATCTGAGGG 1470

Qy   1441 GGAGCGCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530

Qy   1501 TTTTAAAATATATTTTATATAAT 1522
          |||||||||||||||||||||||
Db   1531 TTTTAAAATATATTTTATATAAT 1552
```

RESULT 8
US-09-873-367C-516
Sequence 516, Application US/0987336C
Publication No. US20030165839A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: Soppet, Daniel
APPLICANT: Endress, Gregory
APPLICANT: Augustus, Meena
APPLICANT: Ebner, Reinhard
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US/0987336C
PRIOR APPLICATION NUMBER: US20030165839A1
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: Patentin version 3.0
SEQ ID NO 516
;   LENGTH: 1552
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-873-367C-516

```
Query Match         100.0%;  Score 1522;  DB 10;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy      1 ACAGTCAGCCGCATGGCTC...CCCTGTGCCCCAGCCCCTGGCTCCTCTCGTTGATCCCCGCC    60
          ||||||||||||||||||||...|||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCCGCATGGCTC...CCCTGTGCCCCAGCCCCTGGCTCCTCTCGTTGATCCCCGCC    60

Qy     31 ...                                                                90
Db     31 ...                                                                90
```

(Continuing Qy/Db paired alignment rows from position 1 through 1552, 100% identity.)

```
Qy   1501 TTTTAAAATAAATATTTATAAT                                           1522
          |||||||||||||||||||||
Db   1531 TTTTAAAATAAATATTTATAAT                                           1552
```

```
Query Match         100.0%;  Score 1522;  DB 11;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy      1 ACAGTCAGCCGCATGGCTC...CCCTGTGCCCCAGCCCCTGGCTCCTCTCGTTGATCCCCGCC    60
```

Db   31 ACAGTCAGCCGCATGGCTCCCCGTGCCCACCCTGTGGGG
         |||||||||||||||||||||||||||||||||||||||

(Sequence alignment block — Qy = query, Db = database — positions continue from 31 through 1552)

RESULT 10
US-10-301-822-11
; Sequence 11, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)...(1422)
US-10-301-822-11

Query Match   100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACAGTCAGCCGCATGGCTCCCCGTGCCCACCCTGTGGGGACCTGGGTGACTCTCGGCTACAGCTGAACTTCCGA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db        1 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGATCCCGGCC
Qy
```

```
Qy       31 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGATCCCGGCC 90
            ||||||||||||||||||||||||||||||||||||||||||
Db       61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTTCGATGCCTGTCCAT 120
```

```
Qy       91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTTCGATGCCTGTCCAT 150
Db      121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCTTGGGGAA 180
```

```
Qy      121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCTTGGGGAA 180
Db      151 GATGACCCACTGGGGCGAGGAGGATCTGCCCAGTGAAGAGAAGAGGAGGAT 210
```

```
Qy      151 ...
Db      181 ...
```

(— sequence alignment continues, Qy/Db rows paired with match bars —)

```
Qy     1081 CACACCCTTCTCTGACACCCTGTGGGGACCTGGTTGACTCTCGGGCTACAGCTGACACTTCCGA
Db     1111 CACACCCTTCTCTGACACCCTGTGGGGACCTGGTTGACTCTCGGGCTACAGCTGAACTTCCGA 1170
```

```
Db     1141 GCGGACGCACGCGCTTTGAATGGGCGGCAGCGAGTGATTGAGCGGCTCCTTCCTTCCCTGCTGGAGTTGGACAGC 1200
Qy     1171 GCGGACGCACGCTTTGAATGGGCGGCAGCGAGTGATTGAGCGGCTCCTTCCTTCCCTGCTGGAGTTGGACAGC 1230
```

```
Qy     1201 AGTCCTCGGGCGTCGCTGAGCCAGCCAGCTGAAATTCCTGCGCTGGCGTGCGTGGTGACATCCTA 1260
Db     1231 AGTCCTCGGGCGTCGCTGAGCCAGCCAGCTGAAATTCCTGCGCTGGCGTGCGTGGTGACATCCTA 1290
```

```
Db     1261 GCCCTGGGTTTTTTGGCCTCCTCTTTTTGCTGTCACCAGCGTTGCGTGTCAGATGAGA 1320
Qy     1291 GCCCTGGTTTTTGGCCTCCTCTTTTTGCTGTCACCAGCGTTGCGTGTCAGATGAGA 1350
```

```
Qy     1321 AGGCAGCACAGAGAAGGGGAACCAAAGGGGGTGTGGTTACCGGCCCCAGCAGAGGGTAGCCGAG 1380
Db     1351 AGGCAGCACAGAGAAGGGGAACCAAAGGGGGTGTGGTTACCGGCCCCAGCAGAGGGTAGCCGAG 1410
```

```
Db     1381 ACTGGAGCCTAGAGGCCGTGGATCTTGGAGAATGTGAGAGAGCCAGCCAGCGCCATCTGAGGG 1440
Qy     1411 ACTGGAGCCTAGAGGCCGTGGATCTTGGAGAATGTGAGAGAGCCAGCCAGCGCCATCTGAGGG 1470
```

```
Qy     1441 GGAGCCGGTTAACTGTCCCTGTCCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
Db     1471 GGAGCCGGTTAACTGTCCCTGTCCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530
```

```
Qy     1501 TTTTAAAATAAATAATTTATTAT 1522
Db     1531 TTTTAAAATAAATAATTTATTAT 1552
```

RESULT 11
US-10-465-572-9
; Sequence 9, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.0012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-465-572-9

Query Match 100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        1 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGATCCCGGCC 60
Db       31 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGATCCCGGCC 90
```

```
Qy       61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTTCGATGCCTGTCCAT 120
Db       91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTTCGATGCCTGTCCAT 150
```

```
Qy      121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCTTGGGGAA 180
Db      151 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCTTGGGGAA 210
```

```
Qy      181 GATGACCCACTGGGGCGAGGAGGATCTGCCCAGTGAAGAGAAGAGGAGGAT 240
Db      211 GATGACCCACTGGGGCGAGGAGGATCTGCCCAGTGAAGAGAAGAGGAGGAT 270
```

RESULT 12
US-10-172-118-574
; Sequence 574, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

Query Match   100.0%;   Score 1522;   DB 15;   Length 1552;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy      1 ACAGTCAGCCGCATGGCTTCCCCTGTGCCCCAGCCCTGGCCTCCCTGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTCAGCCGCATGGCTTCCCCTGTGCCCCAGCCCTGGCCTCCCTGTTGATCCCGGCC 90

Qy     61 CCTGCTCCAGGCCCTCACTGTGCAACTCGTCGCTTCACTGCTGCTTCGATGCTGTCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGCCCTCACTGTGCAACTCGTCGCTTCACTGCTGCTTCGATGCTGTCAT 150

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCCTTCTGGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCCTTCTGGGAA 210

Qy    181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAGAAGGATTCACCCAGGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAGAAGGATTCACCCAGGAGGAGGAT 270

Qy    241 CCACCCCGGAGAGGATCTACCTGGACAGAGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCCGGAGAGGATCTACCTGGACAGAGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTT 360
          |||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTT 390
```

```
Qy         361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy         421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510

Qy         481 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         511 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 570

Qy         541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGC 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         571 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGC 630

Qy         601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         631 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 690

Qy         661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         691 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC 750

Qy         721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 810

Qy         781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         811 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 870

Qy         841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         871 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930

Qy         901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990

Qy         961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050

Qy        1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1051 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1110

Qy        1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1111 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1170

Qy        1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1171 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1230

Qy        1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1290

Qy        1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1291 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1350

Qy        1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1351 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1410

Qy        1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1470

Qy        1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1471 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530

Qy        1501 TTTTAAAATAAATATTTATAAT 1522
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Db        1531 TTTTAAAATAAATATTTATAAT 1552
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RESULT 13
US-10-388-360-291
; Sequence 291, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
;  APPLICANT: GENOMIC HEALTH
;  APPLICANT:  Baker, Joffre B.
;  APPLICANT:  Cronin, Maureen T.
;  APPLICANT:  Kiefer, Michael C.
;  APPLICANT:  Shak, Steve
;  APPLICANT:  Walker, Michael Graham
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
;  FILE REFERENCE: 39740-0001US
;  CURRENT APPLICATION NUMBER: US/10/388,360
;  CURRENT FILING DATE:  2003-03-12
;  PRIOR APPLICATION NUMBER: US 60/412,049
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: US 60/364,890
;  PRIOR FILING DATE: 2002-03-13
;  NUMBER OF SEQ ID NOS: 384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 291
;   LENGTH: 1552
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-388-360-291

  Query Match             100.0%;  Score 1522;  DB 15;  Length 1552;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          31 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 90

Qy          61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 150

Qy         121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 210

Qy         181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         211 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 270

Qy         241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy         301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy         361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy         421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510

Qy         481 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 540
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RESULT 14
US-10-295-027-305

; Sequence 305, Application US/10295027
; Publication No. US20030223350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-0125000US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/350,250
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 305
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-305

Query Match   100.0%;   Score 1522;   DB 15;   Length 1552;
Best Local Similarity   100.0%;
Matches 1522;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ACAGTCAGCCGCCATGGCTCCCCCTGTGCCCCAGCCCTGGCTCCCTCCTCTGTTGATCCCCGGCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 ACAGTCAGCCGCCATGGCTCCCCCTGTGCCCCAGCCCTGGCTCCCTCCTCTGTTGATCCCCGGCC 90

Qy   61 CCTGCTCCAGGCCTCACTGTGCAAACTCGCTCACTGCTGGTTCTGATGCCCTGCCAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91 CCTGCTCCAGGCCTCACTGTGCAAACTCGCTCACTGCTGGTTCTGATGCCCTGCCAT 150

Qy 121 CCCCAGGAGTTGCCCCGGCATGGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 151 CCCCAGGAGTTGCCCCGGCATGGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA 210

Qy 181 GATGACCCCACTGGGCGCGAGGAGGAGGATTCCCCAGTGAAGAGGAGGATTCACCCAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 211 GATGACCCCACTGGGCGCGAGGAGGATTCCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 270

Qy 241 CCACCCCGGAGGAGGGATCTACCTGGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||
Db 271 CCACCCCGGAGGAGGGATCTACCTGGAGGAGGATCTACCT 330

Qy 301 GAAGTTAAGCCTAAATCAGAAGAGAAGAGGGGCTCCCTGAAGTTGAGAGGAGGATCTACCTGTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 331 ...

Db 511 GCGGGGCCGGCTTCCAGTCTCCCGGTGGGATATCCGCCCCCAGCTCGGCGGCCTTCTGCCCGGCC 570

Qy 541 CTGCCGCCCCCTGGAACTCCTGGGCTTTCAGCTCTCCCAGAACTGCGCGCCTCGCGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 571 CTGCCGCCCCCTGGAACTCCTGGGCTTTCAGCTCTCCCAGAACTGCGCGCCTCGCGC 630

Qy 601 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 631 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCC 690

Qy 661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCCTGCAGGTCGTCCGGGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 691 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCCTGCAGGTCGTCCGGGC 750

Qy 721 TCGGAGCACACTGTGGAAGGGCCCACCGTTTCCCTGCCCGAGATCCACGTGGTTCACCTCAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 751 TCGGAGCACACTGTGGAAGGGCCCACCGTTTCCCTGCCCGAGATCCACGTGGTTCACCTCAGC 810

Qy 781 ACCGGCCTTTGCCAGAGTTGACGAGGGCCCCGGGGGCCGGGGCCTTGGGCCTGGGTGTTGGCC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 811 ACCGGCCTTTGCCAGAGTTGACGAGGGCCCCGGGGGCCGGGGCCTTGGGCCTGGGTGTTGGCC 870

Qy 841 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 871 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930

Qy 901 GAAGAAAATCGCTCAGGAAGGCTCAGGACTCAGGTCCCAGGACTCAGGACAGTTGCTTCTCGCTTG 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 931 GAAGAAAATCGCTCAGGAAGGCTCAGGACTCAGGTCCCAGGACTCAGGACAGTTGCTTCTCGCTTG 990

Qy 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGGTCTCTGAGACTGTCGCACTC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 991 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGGTCTCTGAGACTGTCGCACTC 1050

Qy 1021 GCCCAGGGGTGTCATCTGGGGACTGGTGACTCTCGGCTACAGCTGAAACTTCCGA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1051 GCCCAGGGGTGTCATCTGGGGACTGGTGACTCTCGGCTACAGCTGAAACTTCCGA 1110

Qy 1081 CACACCCCTCTCTGACACCCGTGGGGGAACGTGGTTGTTTAACCAGACAGTGAGTGCTGAGTGCTTAAGCAGCTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1111 CACACCCCTCTCTGACACCCGTGGGGGAACGTGGTTGTTTAACCAGACAGTGAGTGCTGAGTGCTTAAGCAGCTC 1170

Qy 1141 GCGACCGCAGCCTTTGAATGGGGGCCTCTTCCCTCCTTCCCTCCTTTCTTCGGGCTACAGCTGAACTTCCGA 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1171 GCGACCGCAGCCTTTGAATGGGGGCCTCTTCCCTCCTTCCCTCCTTTCTTCGGGCTACAGCTGAACTTCCGA 1230

Qy 1201 AGTCCTCTCGGGCTTCTGAGCCAGTCCAGCTGAATTCCTGCCTGCTGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1231 AGTCCTCTCGGGCTTCTGAGCCAGTCCAGCTGAATTCCTGCCTGCTGGTGACATCCTA 1290

Qy 1261 GCCCTGGTTGTTTTGGCCTCGCTCCGTTCCTTGTGCAGATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||
Db 1291 GCCCTGGTTGTTTTGGCCTCGCTCCGTTCCTTGTGCAGATGAGA 1350

Qy 1321 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTTGAGCTACACCGGCCGAG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1351 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTTGAGCTACACCGGCCGAG 1410

Qy 1381 ACTGGAGGAGCCTAGAGGCTGGGATCTTGAGAGAATGTGAGAGGCAGCACGCATCTGAGGG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1411 ACTGGAGGAGCCTAGAGGCTGGGATCTTGAGAGAATGTGAGAGGCAGCACGCATCTGAGGG 1470

Qy 1441 GGAGCCCGGTAACTGTCCTGCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1471 GGAGCCCGGTAACTGTCCTGCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530

Qy 1501 TTTTAAAATAAATAATATTTATAAT 1522
          |||||||||||||||||||||||||
Db 1531 TTTTAAAATAAATAATATTTATAAT 1552

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Db   331  GAGTTAAGCTTAAATCAGNAGNAGAGGGGCTCCCTGAGTTAGAGGATCTACTGTT      390
Qy   361  GAGGCTCCTGGGAGATCCTCAAGAACCCAGGAATAATGCCCAGGGACAAAGAAGGGGAT    420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   391  GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT  450
Qy   421  GACCAGAGTCATTGGCGTATGGAGGGGACCCGCCCTGCCCCGGGGTGTCCCAGCCTGC     480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   451  GACCAGAGTCATTGGCGTATGGAGGGGACCCGCCCTGCCCCGGGGTGTCCCAGCCTGC     510
Qy   481  GCGGGGCCGGCCTTCCAGTCCCCGGTGGATAATCCGGCCCCAGCTCGGCCTTCTGCCCGGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511  GCGGGGCCGGCCTTCCAGTCCCCGGTGGATAATCCGGCCCCAGCTCGGCCTTCTGCCCGGCC 570
Qy   541  CTGCGCGCCCCCTGGGAACTCCTGGGGCTTCAGCTCCCGCTCCCAGAACTGCGGCCTGCGC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571  CTCGCGCGCCCCTGGGAACTCCTGGGGCTTCAGCTCCCGCTCCCAGAACTGCGGCCTGCGC  630
Qy   601  AACAATGGCCCACAGTGTGCAACTGACCCCTGCCTCCTGGCTAGAGATGGCTCTGGGGTCCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631  AACAATGGCCCACAGTGTGCAACTGACCCCTGCCTCCTGGCTAGAGATGGCTCTGGGGTCCC 690
Qy   661  GGGCGGGGAGTACCCGGGCCTTCTGCGACTTGCGACTCGGGGGGGGGCTGCAGGTCGTCCGGGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691  GGGCGGGGAGTACCCGGGCCTTCTGCGACTTGCGACTCGGGGGGGGGCTGCAGGTCGTCCGGGC 750
Qy   721  TCCGAGACACACTGTGGAAGGCACCACCGTTTCCCTCGCCGAGATCCACGTGGTTCACCTCAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751  TCCGAGCACACTGTGGAAGGCACCGTTTCCCTCGCCGAGATCCACGTGGTTCACCTCAGC   810
Qy   781  ACCCGCCCTTTGCCAGAGTTGACGAGGGCCCTTGGGGGGGCCCGGGAGGCCCTGGCCGTGTTGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811  ACCCGCCCTTTGCCAGAGTTGACGAGGGCCCTTGGGGGGGCCCGGGAGGCCCTGGCCGTGTTGGGC 870
Qy   841  GCCTTTCTGGGAGAGGGGCCCCGGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTCTTCGGCTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871  GCCTTTCTGGGAGAGGGGCCCCGGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTCTTCGGCTTG 930
Qy   901  GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931  GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC   990
Qy   961  CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCCCTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991  CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCCCTGT  1050
Qy  1021  GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGAATGCTGAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1051  GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGAATGCTGAGTGCTAAGCAGCTC 1110
Qy  1081  CACACCCCTCTCTGACACCCTGTGGGGACCTGGTCGACTCTCCGGCTACAGCTGAACTTCCCA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1111  CACACCCTCTCTGACACCCCGTGGGGACCTGGTCGACTCTCCGGCTACAGCTGAACTTCCCA 1170
Qy  1141  GGGACGCGCAGCCTTTGAATGGGCCAGAGTGATTGAGGCGTCCTCCTTCCCTGCGGAGTGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1171  GCCACGCGCAGCCTTTGAATGGGCCAGAGTGATTGAGGCGTCCTCCTTCCCTGCGGAGTGGACAGC 1230
Qy  1201  AGTCCTCGGGCTGTGAGCCTGAATTCCTGGCTGTGGGCTGTCGGTGACATCCTA      1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1231  AGTCCTCGGGCTGTGAGCCTGAATTCCTGGCTGTGGGCTGTCAGCATCCTA         1290
Qy  1261  GCCCTGGTTTGCTGTCAGGCGTCGCGGTTCCTTGCAGATGAGA              1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1291  GCCCTGGTTTGCTGTCACCAGGCGTCGCGGTTCCTTGCAGATGAGA              1350
Qy  1321  AGGCAGCACAGGAGGGACCAAAGGGGGTGTGTGAGCTACCGCGCCACAGCTAGAGGTAGCCCAG  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1351  AGGCAGCACAGGAGGGAACCAAAGGGGGTGTGTGAGCTACCGCGCCACAGCTAGAGGTAGCCCAG  1410
Qy  1381  ACTGGAGCCTTAGAGGCTGGATCTTGGGAGAATGTGAGAAGCCAGCCAGAGAGGCCATCTGAGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1411  ACTGGAGCCTAGAGGGCTTGGATCTTGGGAGAATGTGAGAAGCCAGCCAGAGAGGCCATCTGAGGG 1470
Qy  1441  GGAGCGCGGGTAACTGGTCGTCCCTGCTCCTGGTCGTCCTCATTATTGCCAGAAATT     1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1471  GGAGCGCGGGTAACTGGTCGTCCCTGCTCCTGGTCGTCCTCATTATTGCCACTTCCTTTAACTGCCAGAAATT 1530
Qy  1501  TTTTAAATAAATATTTATTTAT          1522
          ||||||||||||||||||||||||
Db  1531  TTTTAAATAAATATTTATTTAT          1552
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RESULT 15
US-10-295-027-1022

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; Sequence 1022, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT: Aziz, Natasha
;  APPLICANT: Ginsberg, Wendy M.
;  APPLICANT: Gish, Kurt C.
;  APPLICANT: Glynne, Richard
;  APPLICANT: Hevezi, Peter A.
;  APPLICANT: Mack, David H.
;  APPLICANT: Murray, Richard
;  APPLICANT: Watson, Susan R.
;  APPLICANT: Bos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-0125000US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1022
;  LENGTH: 1552
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-295-027-1022

Query Match             100.0%;  Score 1522;  DB 15;  Length 1552;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1522;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  ACAGTCAGCCGCCATGGCTCCCCTGCCCAGCCCCCTGGCTCCCCTCGTTGGATCCGGGCC    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    31  ACAGTCAGCCGCCATGGCTCCCCTGCCCAGCCCCCTGGCTCCCCTCGTTGGATCCGGGCC    90
Qy    61  CCTGCTCCAGGCCTCACTGTGCAACTGCTGTGCTTCGTGATGCCTGTCCAT          120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    91  CCTGCTCCAGGCCTCACTGTGCAACTGCTGTGCTTCGTGATGCCTGTCCAT          150
Qy   121  CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTTCTGGGGAA 180
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Db   151  CCCAGGAGGTTGCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTGGGGAA 210
                                                              
Qy   181  GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211  GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAGGAT 270

Qy   241  CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||
Db   271  CCACCCGGAGGAGGAGGATCTACCTCTGGAGGAGGAGGATCTACCTT 330

Qy   301  GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAAGGATCTACTTACTGTTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   331  GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAAGGATCTACTTACTGTTT 390

Qy   361  GAGGCTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
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Db   391  GAGGCTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 450

Qy   421  GACCAGAGAGTCATTGGGCGTATGGAGGGGCGACCCCGCCCGGGCCGGGTGTCCCCAGCCTGC 480
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Db   451  GACCAGAGAGTCATTGGGCGTATGGAGGGGCGACCCCGCCCGGGCCGGGTGTCCCCAGCCTGC 510

Qy   481  GCGGGGCCGCTTCCAGTCCCCGGTGGGATATCCGGCCCCCCCAGCTCGGCCGGCCTTCTCCCGGCC 540
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Db   511  GCGGGGCCGCTTCCAGTCCCCGGTGGGATATCCGGCCCCCCCAGCTCGGCCGGCCTTCTCCCGGCC 570

Qy   541  CTGCGCCCCCTGGAACTCCTCGGGCGTTCCAGCTCCCGCGCCTCCAGAACTGCGCCTGCGCG 600
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Db   571  CTGCGCCCCCTGGAACTCCTCGGGCGTTCCAGCTCCCGCGCCTCCAGAACTGCGCCTGCGCG 630

Qy   601  AACAAATGCCACAGTGTGCAACTGACCCCTGCCTCCTCGGCTAGAGATGTGGGTCC 660
          ||||||||||||||||||||||||||||||||||||||
Db   631  AACAAATGCCACAGTGTGCAACTGACCCCTGCCTCCTCGGCTAGAGATGTGGGTCC 690

Qy   661  GGGCGGGGAGTACCCGGCTCTGCAGCTGCATCGCACTGGGGGGGCTGCAGGTCGTCCGGGC 720
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Db   691  GGGCGGGGAGTACCCGGCTCTGCAGCTGCATCGCACTGGGGGGGCTGCAGGTCGTCCGGGC 750

Qy   721  TCCGAGCACACTGTGGAAGGCCACCGTTTCCCGCCGAGATCCAGCTGCCACTGGATCAGC 780
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Db   751  TCGGAGCACACTGTGGAAGGCCACCGTTTCCCGCCGAGATCCAGCTGCCACTGGATCAGC 810

Qy   781  ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCGCCCGGAGGGCCTGGCCCGTGTTGGCC 840
          |||||||||||||||||||||||||||||||||||
Db   811  ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCGCCCGGAGGGCCTGGCCCGTGTTGGCC 870

Qy   841  GCCTTTCTTGGGAGGAGGCCCCGGAAGAAAACAGTGCCTTATGACGCAGTTGCTCGTGTTCGCTTG 900
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Db   871  GCCTTTCTTGGGAGGAGGCCCCGGAAGAAAACAGTGCCTTATGACGCAGTTGCTCGTGTTCGCTTG 930

Qy   901  GAAGAAATCGGCTGAGGAAGGCTCAGAGACTCAGGACTGGACATATCTGCACTC 960
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Db   931  GAAGAAATCGGCTGAGGAAGGCTCAGAGACTCAGGACTGGACATATCTGCACTC 990

Qy   961  CTGCCCCTGACTTCAGCGCGCTACTTCCAAATATGAGGGGTCTTCTGACTACACGCCCCTGT 1020
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Db   991  CTGCCCCTGACTTCAGCGCGCTACTTCCAAATATGAGGGGTCTTCTGACTACACGCCCCTGT 1050

Qy  1021  GCCCAGGGGTGTCATCTGGACTGGTGTTTAACCAGACAGTGATGCTCAGCTGAACTTCCGA 1080
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Db  1051  GCCCAGGGGTGTCATCTGGACTGGTGTTTAACCAGACAGTGATGCTCAGCTGAACTTCCGA 1110

Qy  1081  CACACCCTCTCTGACACCCGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140
          |||||||||||||||||||||||||||||||||||
Db  1111  CACACCCTCTCTGACACCCGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1170

Qy  1141  GCGACGCAGCCCTTTGAATGGGGCGAGTGATTGAGGGCCTCCTTCCCTGCTTACAGCTGGTGGCAGC 1200
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Db  1171  GCGACGCAGCCCTTTGAATGGGGCGAGTGATTGAGGGCCTCCTTCCCTGCTTACAGCTGGTGGCAGC 1230

Qy  1201  AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAATTCCTTGCCTGGCTGCTTGGCTTGGTTGACATCCTA 1260
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Qy  1261  GCCCTGGTTTTTGGCCTCCTTTTTTGGCTCTTCACGTCGGCGTTCCTTGTGCAGATGAGA 1320
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Db  1291  GCCCTGGTTTTTTGGCCTCCTTTTTTGGCTCTTCACGTCGGCGTTCCTTGTGCAGATGAGA 1350

Qy  1321  AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGGCTACGGCCCCAGCAGGGTAGCCGAG 1380
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Db  1351  AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGGCTACGGCCCCAGCAGGGTAGCCGAG 1410

Qy  1381  ACTGGAGCCTAGAGGCTGGGATCTTGGAGAAATGTGAGAAGCCAGCGAGGCCATCTGAGGG 1440
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Db  1411  ACTGGAGCCTAGAGGCTGGGATCTTGGAGAAATGTGAGAAGCCAGCGAGGCCATCTGAGGG 1470

Qy  1441  GGAGCCGGTTAACTGTCCTGCTCATTATCGCCATTCCTTTTAACTGCCAAGAAAATT 1500
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Db  1471  GGAGCCGGTTAACTGTCCTGCTCATTATCGCCACTTCCTTTTAACTGCCAAGAAAATT 1530

Qy  1501  TTTTAAAATAAAATATTTATAAAT 1522
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Db  1531  TTTTAAAATAAAATATTTATAAAT 1552
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Search completed: February 6, 2005, 11:25:27
Job time : 868 secs

OM nucleic - nucleic search, using sw model

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                            GenCore version 5.1.6
                     Copyright (c) 1993 - 2005  Compugen Ltd.

Run on:            February 6, 2005, 07:10:26 ; Search time 4446 Seconds
                                              (without alignments)
                                              12474.420 Million cell updates/sec

Title:          US-09-967-237A-1
Perfect score:  1522
Sequence:       1 acagtcagccgcatggctcc...........ttaaaataatatattataat 1522
Scoring table:  OLIGO NUC
                Gapop 60.0 , Gapext 60.0
Searched:       32822875 seqs, 1821965908 residues
Word size :     50

Total number of hits satisfying chosen parameters:          84

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries
Database :      EST:*
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                2: gb_est2:*
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                9: gb_gss2:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                   SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	1461	96.0	1541	3	CR597234	CR597234 full-leng
2	1453	95.5	1523	3	CR620502	CR620502 full-leng
3	1418	93.2	1169	3	CR616345	CR616345 full-leng
4	1171	76.9	1492	3	CR590646	CR590646 full-leng
5	839	55.1	1009	1	AL558378	AL558378 full-leng
6	825	54.2	1084	1	AL542336	AL542336
7	757	49.7	1017	5	BX401186	BX401186
8	635	41.7	927	1	AL555184	AL555184
9	619	40.7	1070	4	AL554705	AL554705
10	617	40.5	874	4	BG386425	BG386425 602455652
11	555	36.5	669	1	AI925646	AI925646 wo32d07.x
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13	531	34.9	627	6	BM529941	BM529941 AGENCOURT
14	526	34.6	659	6	CA416326	CA416326 UI-H-FE0-
15	514	33.8	682	1	AI831707	AI831707 wj40h01.x
16	508	33.4	668	4	BG824243	BG824243 602729440
17	502	33.0	691	5	BU620600	BU620600 UI-H-FL1-
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22	435	28.6	618	5	AW615291	AW615291 hh40f01.x
23	428	28.1	577	1	AI032380	AI032380 ov37e07.x
24	424	27.9	438	2	AW449513	AW449513 UI-H-BI3-
25	416	27.3	4512	3	BC038673	BC038673 Homo sapi
26	407	26.7	658	2	AI769526	AI769526 wj24a11.x
27	404	26.5	579	1	AI402286	AI402286 tg43c07.x
28	390	25.6	836	5	BX383092	BX383092 K-EST0098
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32	373	24.5	465	2	AW293135	AW293135 UI-H-B12-
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36	354	23.3	352	7	CK903817	CK903817 1e66d01.x
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38	319	21.0	438	2	AW612951	AW612951 hh39c11.x
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40	312	20.5	328	4	BI964215	BI964215 1e66d01.y
41	308	20.2	727	5	BX370540	BX370540 1e67f08.x
42	307	20.2	328	4	BM052891	BM052891 BX370540.Y
43	305	20.0	543	1	AA879425	AA879425 oj91d02.s
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                                  ALIGNMENTS

RESULT 1
LOCUS           CR597234
DEFINITION      CR597234                1541 bp    mRNA    linear   HTC 21-JUL-2004
                full-length cDNA clone CS0DI085YF18 of Placenta Cot 25-normalized
                of Homo sapiens (human).
ACCESSION       CR597234
VERSION         CR597234.1              GI:50478041
KEYWORDS        HTC; CNSLT cDNA.
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 1541)
  AUTHORS       Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE         Full-length cDNA libraries and normalization
  JOURNAL       Unpublished
  REMARK        Contact : Feng Liang Email : filang@lifetech.com URL :
                http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
                Faraday Avenue
REFERENCE       2  (bases 1 to 1541)
  AUTHORS       Genoscope.
  TITLE         Direct Submission
  JOURNAL       Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT         1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
                end enriched, double-strand cDNA was digested with Not I and cloned
                into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                was normalized. Library was constructed by Life Technologies, a
                division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..1541
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone="CS0DI085YF18"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match        96.0%;  Score 1461;  DB 3;  Length 1541;
Best Local Similarity   99.9%;
Matches 1511;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy     1 ACAGTCAGCCGCATGGCTCCCTCCCCTGTGCCCCAGCCCCTGGGCTCCCTCCGTTGATCCCGGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    30 ACAGTCAGCCGCATGGCTCCCTCCCCTGTGCCCCAGCCCCTGGGCTCCCTCCGTTGATCCCGGCC 89
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Qy    61 CCTGCTTCCAGGCCTCACTGTGCAAACTGCTGCTTCTGAATGCCTGTCCAT 120
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Db    90 CCTGCTTCCAGGGCCTCACTGTGCAAACTGCTGCTTCTGGTGCCTGTCCAT 149

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCTTGGGAGGAGGGAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCTTGGGGAGGGGGAA 209

Qy   181 GATGACCCACTGGGCGGGAGGGAGTCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   210 GATGACCCACTGGGCGGGAGGGATCTGCCCAGTGAAGAGGATCTCACCCAGAGGAGGAT 269

Qy   241 CCACCCCGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
         ||||||||||||||||||||||||||||||||||||||||||
Db   270 CCACCCCGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 329

Qy   301 GAAGTTAAGCCTAAATCAGAGAGAAGAGGCTCCCTGGAGGTTAGAGGATCTACTACTGTT 360
         ||||||||||||||||||||||||||||||||||||||||||||
Db   330 GAAGTTAAGCCTAAATCAGAGAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACTACTGTT 389

Qy   361 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGAT 420
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Db   390 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGAT 449

Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGGCCGACCCCCGCCCGGGGTGTCCCCAGCCTGC 480
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Db   450 GACCAGAGTCATTGGGCGCTATGGAGGGCCGACCCCCGCCCGGGGTGTCCCCAGCCTGC 509

Qy   481 GCGGGGCCGCCTTCCAGTCCCGGGGATATCCGCGCCCGCCTTCTGCCCGGCC 540
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Db   510 GCGGGGCCCTTCCAGTCCCGGGGATATCCCGCGCCCAGCTCTGCCCGGCC 569

Qy   541 CTGCGCCCCCTTGGAACTCTCGGGGCTTCCAGCTCCCGGGGAACTGCGCCTCTCGCC 600
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Db   570 CTGCGCCCCCTTGGAACTCTCGGGGCTTCCAGCTCCCGGGGAACTGCGCCTCTCGCC 629

Qy   601 AACAATGGCCACAGTGTGTCAAACTGACACCCTGCCTCCTGGGATGGTCTTGGGGTCCC 660
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Db   630 AACAATGGCCACAGTGTGTCAAACTGACACCCTGCCTCCTGGGATGGTCTAGGGGTCCC 689

Qy   661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCGCAGGTCGTCTCCGGGC 720
         |||||||||||||||||||||||||||||||||||||||||
Db   690 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCGCAGGTCGTCTCCGGGC 749

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGCGTTTCCCCTGCCGGTCGTTCACCTCAGC 780
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Db   750 TCGGAGCACACTGTGGAAGGCCACCGCGTTTCCCCTGCCGAGATCCACGTTCACCTCAGC 809

Qy   781 ACGGCCCCTTGCCAGAGTTGACGAGGGCCCTTGGGGCGGCCCTGGGGGCGGCCGCC 840
         |||||||||||||||||||||||||||||||||||||||||
Db   810 ACGGCCCTTGCCCAGAGTTGACGAGGGCCCTTGGGGCGGCGCCGGGCCGGCCGCC 869

Qy   841 GCCTTTCTGGACAGCAGTGGTCCAGTGCCTATGAGCAGTTGAGCAGTTGTCTCGGCTTG 900
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Db   870 GCCTTTCTGGAGCAGGGCCGGAGAAAAACAGTGCCCTATGAGCAGTTGTCTCGGCTG 929

Qy   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTGCTCCAGCTGGACATATCTGCACTC 960
         |||||||||||||||||||||||||||||||||||||||||
Db   930 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTGCTCCAGCTGGACATATCTGCACTC 989

Qy   961 CTGCGCCCTCTGACTTCAGCGCGTACTTCCAAATGATGAGGGGGTCTCTGACTACACCGGTT 1020
         |||||||||||||||||||||||||||||||||||||||||
Db   990 CTGCGCCCTCTGACTTCAGCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACCGGTGT 1049

Qy  1021 GCCCAGGGTGTCATCTCGGACTGTGTTTAACCAGACAGTGATGCTGCTGAGTGCTAAGCACAGTC 1080
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Db  1050 GCCCAGGGTGTCATCTCGGACTGTGTTTAACCAGACAGTGATGCTGCTGAGTGCTAAGCACAGTC 1109

Qy  1081 CACACCCTCTCTGACACCCGTGGGGGACCTGGTTGACTCTCGGGCTACAGTGAACTTCCGA 1140
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Db  1110 CACACCCTCTCTGACACCCGTGGGGGACCTGGTTGACTCTCGGGCTACAGTGAACTTCCGA 1169

Qy  1141 GCGACGCAGCCTTTGAAATGGGCGAGTGATTGAGGGCCTTCCCTGCCTCTGGTGTGGAGTGGCACAGC 1200
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Db  1170 GCGACGCAGCCTTTGAATGGGCCAGCGAGTGATTGAGGGCCTTCCCTGCCTCTGGTGTGGAGTGGCACAGC 1229

Qy  1201 AGTCCTCGGGCTGCTTGAGGCCAGTCCAGTGAATTCCTGCCTGGGCTGTGCTGGGTGTGACATCCTA 1260
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Qy  1261 GCCCTGGGTTTTTGGCCTCCTTTTTTGCTGTCAGCCAGCGTGCGGTTCCTTGTGCAGATGAGA 1320
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Db  1290 GCCCTGGGTTTTTGGCCTCCTTTTTTGCTGTCACAGGCGTGCGGTTCCTTGTGCAGATGAGA 1349

Qy  1321 AGGGCAGCAGAGAAGCGGGAACCAAAAGGGGTGTGAGCGTACCGGCCCACAGCGAGAGGTAGCCGAG 1380
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Db  1350 AGGGCAGCAGAGAAGCGGGAACCAAAAGGGGTGTGAGCTACCGGCCCAGAGGTAGCCGAG 1409

Qy  1381 ACTGGAGGCCTAGGACTGATCTGGAGAATGTGGAGAAGCCAGCAGGCATCTGAGGG 1440
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Db  1410 ACTGGAGGCCTAGGACTGATCTTGGAGAATGTGAGAGCCAGCAGGCATCTGAGGG 1469

Qy  1441 GGAGCCCGGTAACTGTCCCGTGTCCCTGCTCATTATGCCACTTCCTTTTTTAACTGCCAGAAATT 1500
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Qy  1501 TTTTAAAATAAA 1512
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Db  1530 TTTTAAAATAAA 1541
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RESULT 2
CR620502

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LOCUS       CR620502                1523 bp    mRNA    linear    HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DK007YK10 of Hela cells Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR620502
VERSION     CR620502.1  GI:50501309
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1523)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact: Feng Liang Email: fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1523)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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ORIGIN
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Best Local Similarity  99.9%;   Pred. No. 0;
Matches 1503;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
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Qy     61 CCTGCTCCCAGGGCCTCACTGTGCAACTGCTGTGCCCCAGCCCCTGTCCCCTGTTGATCCCGGCC 120
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Qy    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGACGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
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Db    140 CCACCCGGAGGAGGGAGGATCTACCTGGAGGAGGATCTGGGGAGGAGGCTCTTCTGGGGGAA 199

Qy    181 GATGACCCACTGGGGCGGAGGATCTGCCCAGTCTGACGAGGATTCACCCAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 GATGACCCACTGGGGCGGAGGATCTGCCCAGTCTGACGAGGATTCACCCAGAGGAGGAT 259

Qy    241 CCACCCGGAGGAGGGAGGGATCTACCTGGAGGAGGATCTACCT 300
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Db    260 CCACCCGGAGGAGGGAGGGATCTACCTGGAGGAGGATCTACCT 319

Qy    301 GAAGTTAAGCCTAAAATCAGAAGAAGAGAGGGAGGGCTCCCTGAAGTTAAGCCTAAAATCAGAGA 360
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Db    320 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGAGGGCTCCCTGAAGTTAGACTCCTACTGTT 379

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Db    380 GAGGCTCCTCGGAGATCCTCAAGAACCCCAGAATAAATGCCACAGGGACAAAAGAAGGGAT 439

Qy    421 GACCAGAGTCATTGGGCTATGGAGGGGGACCCCCGCCCTGGCCCTGGCGTGTCCCCAGCCTGC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440 GACCAGAGTCATTGGGCTATGGAGGGGGACCCCCGCCCTGGCCCTGGCGTGTCCCCAGCCTGC 499

Qy    481 GCGGGGCCGCCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCGCCCTTCTGCCCGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500 GCGGGGCCGCCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCGCCCTTCTGCCCGCC 559

Qy    541 CTGCGCCCCCCCTGGAACTCCTGGGCTTCAGCTCCCCGCGCCCCCCAGCTCGCGCCCTGGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560 CTGCGCCCCCCCTGGAACTCCTGGGCTTCAGCTCCCCGCGCCCCCAGCTCGCGCCCTGGC 619

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGGGCGCCTTCCTCCGGGACTGGCTAGAGATGGC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    620 AACAATGGCCACAGTGTGCAACTGACCCTGCGCTCCCTCTGGGCTAGAGATGGCTCTGGGTCC 679

Qy    661 GGGCCGGGAGTACCGGGGCGCTCTGCAGCTGCATCTCGGGGGGCTGCAGGTCGTGCCGGGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    680 GGGCCGGGAGTACCGGGGCTCTGCAGCTGCATCGCCGGGGGCTGCAGGTCGTGCCGGGC 739

Qy    721 TCGGAGCACACTGTGGAAGGGCCACACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    740 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 799

Qy    781 ACGGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCGGCCCTGGCCGGGAGCCTGGCCTGGCC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    800 ACGGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCGGCCCTGGCCGGGAGCCTGGCCTGGCC 859

Qy    841 GCCTTTCTGGAGGAGGGCGGCGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCGGTTG 900
          ||||||||||||||||||||||| |||||||||| |||||||||||||||||||||
Db    860 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCGGTTG 919

Qy    901 GAAGAAAATCGGCTGAGGAAGGGCTCAGAGAGACTCAGGTCCCAGGACTGGACATGAGCGGGT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    920 GAAGAAAATCGGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 979

Qy    961 CTGCCCTCTGACTTCAGCGGCTACTTCATTCAAATATGAGGGGGTCTTGACTACACACCCCTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    980 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGTCTTGACTACACACCCCTGT 1039

Qy   1021 GCCCAGGGCTGTCATCTGACTGTGTTTAACCAGACAGTCGATGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1040 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGCTGAGTGTGCTAAGCAGCTC 1099

Qy   1081 CACACCCTTCTCTGACACCGTGTGGGGACCTGGTTGCACTCTCGGCTACAGCTGGAACTTCCGA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1100 CACACCCTCTCTGACACCGTGTGGGGACCTGGTTGCACTCTCGGCTACAGCTGGAACTTCCGA 1159

Db   1141 GCGGACGCACGCCTTTGAAATGGGGCGGAGTGATTGAGGCGCTCTTCCTTCCCTGGCTGGACAGC 1200
Db   1160 GCGACGCAGCCTTTGAAATGGGGCGGAGTGAATTGAGGCGCTCTTCCTTCCCTGGCTGGACAGC 1219
Db   1201 AGTCCCTCGGCGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGGCCTGCTGTGGTGACATCCTTA 1260
Db   1220 AGTCCTCGGCGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGGCCTGCTGTGGTGACATCCTTA 1279
Db   1261 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGTGTCACCAGCGTCGCGGTTCCTTGTGTGCAGATGA 1320
Db   1280 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGTGTCACCAGCGTCGCGGTTCCTTGTGTCCAGATGAGA 1339
Db   1321 AGGCAGCACAGAAGGGACACCAAAGGGGGTGTGAGCTACGGCCACCGAGGGTACCCGAG 1380
Db   1340 AGGCAGCACAGAAGGGGACACCAAAGGGGGTGTGAGCTACGGCCCAGAGGTAGCCCGAG 1399
Db   1381 ACTGGAGCCTAGAGGCCTGCTGGATCTTGGAGAATGTGAGAAGCCAGCGTGCCGTGCGGTTCTGGTTCCAGATGTGGCCATCTGAGGG 1440
Db   1400 ACTGGAGCCTAGAGGCCTGGATCTTGGAGAATGTGAGAAGCCAGCGTGCCGTGCGGTTCTTGGTTCCAGATGTGGCCATCTCGAGGG 1459
Db   1441 GGAGCCGGTAACTGTCCTGCTGCCGCTCCTTTTTAACTGCCAAGAAATT 1500
Db   1460 GGAGCCGGTAACTGTCCGTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1519

Qy   1501 TTTT 1504
          ||||
Db   1520 TTTT 1523
```

RESULT 3
CR616345

```
LOCUS       CR616345              1469 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DA003YB12 of Neuroblastoma of Homo
            sapiens (human).
ACCESSION   CR616345
VERSION     CR616345.1  GI:50497152
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1469)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Peng Liang Email : filiang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1469)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..1469
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DA003YB12"
                     /tissue_type="Neuroblastoma"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match          93.2%;  Score 1418;  DB 3;  Length 1469;
```

```
Best Local Similarity  99.9%;  Conservative  0;  Pred. No. 0;  Mismatches  1;  Indels  0;  Gaps  0;
Matches 1468;

Qy      9  CCGCATGGCTCCCCGTGCCCCAGCCCCTGCTCCCCTGTTGATCCCGGCCCCTGCTCC     68
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CCGCATGGCTCCCCGTGCCCCAGCCCCTGCTCCCCTGTTGATCCCGGCCCCTGCTCC     60

Qy     69  AGGCCCTCACTGTGTGCAACTGCTCGTGCTCTGATGCCCATCCCCAGAG          128
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AGGCCCTCACTGTGTGCAACTGCTCGTGCTCTGATGCCCATCCCCAGAG          120

Qy    129  GTTGCCCCGGATGCCAGAGAGGAATTCCCCCCTTTGGGGTGGGAAGGATGACCC      188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  GTTGCCCCGGATGCCAGAGAGGAATTCCCCCCTTTGGGGTGGGAAGGATGACCC      180

Qy    189  ACTGGGGCGGAGGAGGATCTGCCCCACTGAGTGAAGAGGATTCACCCAGAGGAGGATCCACCCGG  248
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ACTGGGGCGGAGGAGGATCTGCCCCACTGAGTGAAGAGGATTCACCCAGAGGAGGATCCACCCGG  240

Qy    249  AGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTGAAGTTAA    308
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTGAAGTTAA    300

Qy    309  GCCTAAATCAGAGAAGAGAAGAGGGGCTCCCTGAAGTTAGAGGAGGGCTCC        368
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  GCCTAAATCAGAGAAGAGAAGAGGGGCTCCCTGAAGTTAGAGGAGGGCTCC        360

Qy    369  TGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGGAAAAGAAGGGATGACCAGAG  428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  TGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGATGACCAGAG  420

Qy    429  TCATTGGCGCTATGGAGGCGACCCGGCCCCTGGCCTGGCCTGGCCTGGCGCGG      488
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  TCATTGGCGCTATGGAGGCGACCCGGCCCCTGGCCTGGCCTGGCCTGGCGCGG      480

Qy    489  CTTCCCAGTCCCCGGGTGGATATCCGCGCCCTTCTGCCCGGCCCCTGCGCC       548
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CTTCCCAGTCCCCGGGTGGATATCCGCGCCCTTCTGCCCGGCCCCTGCGCC       540

Qy    549  CCTGGGAACTCCTGGGCCTTCCAGCTCTCCCGCCGCTCCCCAGAACTTGCGCCTGGCCAACAATGG  608
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCTGGAACTCCTGGGCCTTCCAGCTCTCCCGCCGCTCCCCAGAACTTGCGCCTGGCCAACAATGG  600

Qy    609  CCACAGTGTGCAACTGACCCTGCCTCCTGGGGGTTAGAGATGGCTCTGGGGTCCCGGGGCGGA    668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CCACAGTGTGCAACTGACCCTGCCTCCTGGGGGTTAGAGATGGCTCTGGGGTCCCGGGGCGGA    660

Qy    669  GTACCCGGGCGCTCGCAGCTGCATCTGCACTGCAGGTCGTCGTCCGGAGCGCTCGGAGCA   728
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  GTACCCGGGCGCTCGCAGCTGCATCTGCACTGCAGGTCGTCGTCCGGAGCGCTCGGAGCA   720

Qy    729  CACTGTGGGAAGGCCACCCGTTTCCCCTGCCGTTCCCGAGGGTTCACCTCAGCGACCGGCCTT  788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CACTGTGGAAGGCCACCCGTTTCCCGCGAGATCCACGTGGTTCACCTCAGCGACCGGCCTT  780

Qy    789  TGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGGGCCTGGGCGTTGGGGCCCTTTCT      848
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGGGCCTGGGCGTTGGGGCCCTTTCT      840

Qy    849  GGAGGAGGGGCTGCCCCGGAAGAAGAAAAACAGTGCCTTATGACAGTTGCTGTCTCGTC     908
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  GGAGGAGGGGCTCTGCAGCTGCCTATGAGCAGTTGTTGCTGTCTCGTCGCGTTGGACGAGAAAT  900

Qy    909  CGCTGAGGAAGGCTCAGAGACTCAGGTTCCCAGGACATTATCTCCACTCCTCGCCCTC      968
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CGCTGAGGAAGGCTCAGGACTCAGGTTCCCAGGACATTATCTCCACTCCTCGCCCTC      960

Qy    969  TGACTTCAGCGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCGTGCCCAGGG     1028
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TGACTTCAGCGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCGTGCCCAGGG     1020

Qy   1029  TGTCATCTCGGACTGTGTTTAACCAGACAGTAGCTGAGTGCTGTAAGCAGCTTCCACACCCT    1088
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TGTCATCTCGGACTGTGTTTAACCAGACAGTAGCTGAGTGCTGTAAGCAGCTTCCACACCCT    1080

Qy   1089  CTCCTGACACCCCTGTGGGGACCTTGGGTGACTCTCCGCTCACAGCTGACTCACAGTGTCCGGACGGCA   1148
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CTCTGACACCCGTGGGGACCTTGGGTGACTTCTCGGCTCACAGCTGACAACTTCCGAGCGGCA    1140

Qy   1149  GCCTTTGAATGGGGCGGAGTGAATGACGCCTCCTTCCTCCCGCTGGGAGTGGGACAGCAGTCCTCG     1208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GCCTTTGAATGGGGCGGAGTGAATGACGCCTCCTTCCTCCCGCTGGGAGTGGGACAGCAGTCCTCG     1200

Qy   1209  GGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCGTCGGGTTGGGTGACATCCCCTGGT     1268
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCGTCGGGTTGGGTGACATCCCCTGGT     1260

Qy   1269  TTTTGGGCCCTCCTTTTTGCTGTGTCACCAGCGGTCGCGGGTTCCTTTGTGCAGATGAGGAGGCAGCA    1328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TTTTGGGCCCTCCTTTTTGCTGTGTCACCAGCGGTCGCGGGTTCCTTTGTGCAGATGAGGAGGCAGCA    1320

Qy   1329  CAGAAGGGGGAACCAAAGGGGTGTAGCTACCGCCCAGCAGAGTAGCCGGAGACTGGGAGC    1388
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CAGAAGGGGAACCAAAGGGGTGTAGCTACCGCCCAGCAGAGTAGCCGGAGACTGGGAGC    1380

Qy   1389  CTAGAGGCGGGATCTTGAGAAGTGTGAGAAGCCAGCCAGGGGCCAGAGACTGGGAGGGGCCCG   1448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTAGAGGCGGGATCTTGGGAAGAATGTGAGAAGCCAGCCAGGGCCAGAGACTGGGAGGGGCCCG    1440

Qy   1449  TAACTGTCCTGTCCTGCTCATTATGCCAC     1477
           |||||||||||||||||||||||||||||
Db   1441  TAACTGTCCTGTCCTGCTCATTATGCCAC     1469
```

RESULT 4
CR590646

```
LOCUS       CR590646                1492 bp    mRNA      linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DJ005YK14 of T cells (Jurkat cell line)
            Cot 10-normalized of Homo sapiens (human).
ACCESSION   CR590646
VERSION     CR590646.1  GI:50471453
KEYWORDS    HTC; CNSLT cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1492)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1492)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..1492
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ005YK14"
                     /tissue_type="T cells (Jurkat cell line) Cot
                     10-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match             76.9%;  Score 1171;  DB 3;  Length 1492;
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Best Local Similarity 99.9%; Conservative  0; Pred. No. 0; Mismatches  1; Indels  0; Gaps  0;
Matches 1221;

Qy      1 ACAGTCAGCCGCCATGGCTCCCCCTGTCCCCCTGTTGATCCCGGCC                60
          ||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCCGCCATGGCTCCCCCTGTGCCCCCTGTTGATCCCGGCC               60

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGCCTGTCCAT              120
          ||||||||||||||||||||||||||||||||||||||||||||||
Db     31 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGCCTGTCCAT              150

Qy    121 CCCCAGAGGGTTGCCCCGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAA             180
          |||||||||||||||||||||||||||||||||||||||||||||
Db         CCCCAGAGGGTTGCCCCGGAGGATGCGAGGAGGAGGAGGAGGGGGAA             180

Qy    151 CCCCAGAGGGTTGCCCCGGAGGATGCGAGGAGGAGGAGGAGGGGGAA             210
          |||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCCACTGGGGCGGCGGAGGGGGATCTGCCCAGTGAAGGAGGAT           270

Qy    181 GATGACCCCACTGGGGCGGCGGAGGGGGATCTGCCCAGTGAAGGAGGAT           240
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACCCCGGAGGAGGGGGATCTACCTGGGAGGGAGGATCTACCT               300

Qy    211 GATGACCCCACTGGGGCGGCGGAGGGGGATCTGCCCAGTGAAGGAGGAT           270
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCCGGAGGAGGGGGATCTACCTGGGAGGGAGGATCTACCT               330

Qy    241 CCACCCCGGAGGAGGGGGATCTACCTGGGAGGGAGGATCTACCT               300
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGG           360

Qy    271 CCACCCCGGAGGAGGGGGATCTACCTGGGAGGGAGGATCTACCT               330
          |||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAATCAGAAGGAAGAGGAGGCTCCCCTGAAGTTAGG           390

Qy    301 GAAGTTAAGCCTAAATCAGAAGGAAGAGGAGGCTCCCTGAAGTTAGG            360
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGG           420

Qy    331 GAAGTTAAGCCTAAATCAGAAGGAAGAGGAGGCTCCCCTGAAGTTAGG           390
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGG           450

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGG           420
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GACCAGAGTCATTGGCGTATGGAGAGGAGGAGGACCGACTCCCTGGCTG          480

Qy    421 GACCAGAGTCATTGGCGTATGGAGAGGAGGAGGACCGACTCCCTGGCTG          480
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    451 GCCGGGCCGCCTTCCAGTCCCGGTGGATATCCGCCGCCGCCGCCCCGGCC         510

Qy    451 GCCGGGCCGCCTTCCAGTCCCGGTGGATATCCGCCGCCGCCGCCCCGGCC         510
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GCGGCCGAGAGTACCCGGCTTCCAGTCGGAATATCCGCCGCCCTTCCGCC         570

Qy    481 GCGGCCGAGAGTACCCGGCTTCCAGTCGGAATATCCGCCGCCCTTCCGCC         540
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGCGCCCCCTTGGAACTCCTGGGCTTCAGCGTCCCCGACCTCCCCAGC        600

Qy    541 CTGCGCCCCCTTGGAACTCCTGGGCTTCAGCGTCCCCGACCTCCCCAGC          600
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    571 CTGCGCCCCCTTGGAACTCCTGGGCTTCAGCGTCCCCGACCTCCCCAGC        630

Qy    571 CTGCGCCCCCTTGGAACTCCTGGGCTTCAGCGTCCCCGACCTCCCCAGC          630
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACAATGGCCACAGTGTGCAACTGACCCTGCTTCCTGCTTCCTCGGGGTCCC       660

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCTTCCTGCTTCCTCGGGGTCCC        660
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GGGGCGGGAGTACCGGGCTCTGCAGCTGCAGTCGCAGGTCGTCCCGGGC        690

Qy    631 GGGGCGGGAGTACCGGGCTCTGCAGCTGCAGTCGCAGGTCGTCCCGGGC          690
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGGCGGGAGTACCGGGCTCATCTGCAGCTGCAGGTCGTCCCGGGC           720

Qy    661 GGGGCGGGAGTACCGGGCTCATCTGCAGCTGCAGGTCGTCCCGGGC            720
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    691 TCGGAGCACACTGTGGAAGGGGATCCACCGTTTCCCGGAGATCCACGGT        750

Qy    721 TCGGAGCACACTGTGGAAGGGGATCCACCGTTTCCCGGAGATCCACGGT          780
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCGGAGTTCACCTCAGC          810

Qy    751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCGGAGTTCACCTCAGC           810
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACCGGCCCTTTGCCAGAGTTGACGAGGCCTTGGCCGCCCGGCCGGCCC         840

Qy    781 ACCGGCCCTTTGCCAGAGTTGACGAGGCCTTGGCCGCCCGGCCGGCCC          840
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ACCGCCTTGCCAGAGTTGACGAGGCCTTGGCCGCCCGGCCGGCCC           870

Qy    841 GCCTTTTCTGGAGGAGGGAAAGAAAAACAGTGCCTATGAGCAGTTGCTTCTCGGCTTG       900
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTTCTGGAGGAGGGGGAAGAAAAACAGTGCCTATGAGACAGTTGCGTCTCGCTTG     930

Qy    901 GAAGAAAATCGCTGAGGAGAGGCTCAGGACTCAGGTCCCAGGACATAACTGCACTC       960
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    931 GAAGAAAATCGGCTGAGGAGAGGCTCAGGACTCAGGTCCCAGGACATATCTGCACTC      990

Qy    961 CTGCCCTCTTGACTTCAGCGGCTACTTCCAATATGAGGGGTCTCTGACTGCCCCTGT       1020
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGCCCTCTTGACTTCAGCGGCTACTTCCAAATATGAGGGGTCTCTGACTGCCCCTGT    1050

Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTACCAGAGCAGTGATGCTGAGTGAGTCAGCTC      1080
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GCCCAGGGTGTCATCTGGACTGTGTTTACCAGAGCAGTGATGCTGAGTGAGTCAGCTC    1110

Qy   1081 CACACCCTCTTCTGACACCCTGTGGGGACCTGTGGGGGACCTGGTGACTCTCGGGTACT   1140
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 CACACCCTCTTCTGACACCCTGTGGGGACCTGTGGGGGACCTGGTGACTCTCGGACTACTCCGA  1170

Qy   1141 GCGACGACCACCCTTTGAAATGGGGCGAGTGATTGAGCGGCTCCTCCTTCCTGGAGTGGACAGC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 GCGACGCAGCCCTTTGAAATGGGGCGAGTGATTGAGCGGCCTCCTTCCCGCTGGAGTGACAGC   1230

Qy   1201 AGTCCTCCGGGCTGCTGAGCCAG                                         1222
          ||||||||||||||||||||||
Db   1231 AGTCCTCCGGGCTGCTGAGCCAG                                         1252
```

RESULT 5
AL558378

```
LOCUS       AL558378                1009 bp    mRNA    linear   EST 02-APR-2004
DEFINITION  AL558378 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
            Homo sapiens cDNA clone CS0DJ005YK14 5-PRIME, mRNA sequence.
ACCESSION   AL558378
VERSION     AL558378.3  GI:46183776
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1009)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:13280177.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5300.f.
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DJ005BF07QGP1&c=5300.f.
FEATURES             Location/Qualifiers
     source          1..1009
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ005YK14"
                     /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
                     /cell_line="JURKAT"
                     /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
                     10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

```
Query Match             55.1%;  Score 839;  DB 1;  Length 1009;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  839;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ACAGTCAGCCGCCATGGCTCCCCCTGTCCCCCTGTTGATCCCGGCC                60
        ||||||||||||||||||||||||||||||||||||||||||||||
Db   31 ACAGTCAGCCGCCATGGCTCCCCCTGTCCCCCTGTTGATCCCGGCC                90

Qy   61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGCCTGTCCAT              120
        ||||||||||||||||||||||||||||||||||||||||||||||
Db   91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGCCTGTCCAT              150

Qy  121 CCCCAGAGGGTTGCCCCGGAGGATGCGAGGAGGAGGAGGAGGGGGAA              180
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCCCAGAGGGTTGCCCCGGAGGATGCGAGGAGGAGGAGGAGGGGGAA              180
```

RESULT 6
ALS42336

```
LOCUS       ALS42336               1084 bp    mRNA    linear
DEFINITION  ALS42336 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YB19
                EST 24-MAR-2004
ACCESSION   ALS42336
VERSION     ALS42336.3  GI:45717912
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1084)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polyes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:30547384.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a Not I-oligo(dT) primer. Five prime
            end and enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 8734.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DE010CA10QP2&c=8734.f.
FEATURES             Location/Qualifiers
     source          1..1084
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clones="CS0DE010YB19"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a Not I-oligo(dT) primer. Five prime end and enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN
```

```
Query Match     54.2%;  Score 825;  DB 1;  Length 1084;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches   925;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;
```

(Nucleotide sequence alignment — Qy = query, Db = database subject. Paired alignment rows with match bars and position numbers:)

Left alignment block — positions 151 to 869; Right alignment block — positions 18 to 797.

```
RESULT 7

LOCUS       BX401186               1017 bp    mRNA    linear   EST 29-APR-2004
DEFINITION  BX401186 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.
ACCESSION   BX401186
VERSION     BX401186.2  GI:46876709
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1017)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30626393.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5300.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DK009DH05QP1&c=5300.f.
FEATURES             Location/Qualifiers
     source          1..1017
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK009YP10"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match 49.7%; Score 757; DB 5; Length 1017;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 807; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
RESULT 8

LOCUS       AL555184                927 bp    mRNA    linear   EST 30-MAR-2004
DEFINITION  AL555184 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK007YK10 5-PRIME, mRNA sequence.
ACCESSION   AL555184
VERSION     AL555184.3  GI:45859924
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31276593.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
```

RESULT 9
AL554705

LOCUS   AL554705   1070 bp   mRNA   linear   EST 30-MAR-2004
DEFINITION   AL554705 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
             clone CS0DI085YF18 5-PRIME, mRNA sequence.
ACCESSION   AL554705
VERSION   AL554705.3 GI:45859455
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1070)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:31276515.
             Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
             1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
             was normalized. Library was constructed by Life Technologies, a
             division of Invitrogen. This sequence belongs to sequence cluster
             5300.f.
             For more information about this cluster, see
             http://www.genoscope.cns.fr/cdna?s=CS0DI085DC09QP1&c=5300.f.
FEATURES   Location/Qualifiers
     source   1..1070
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI085YF18"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
        1..1070

Query Match   40.7%; Score 619; DB 1; Length 1070;
Best Local Similarity   99.9%; Pred. No. 3.5e-306;
Matches 669; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCTGGCTCCCTCTGGTTGATCCCCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCTGGCTCCCTCTGGTTGATCCCCGGC 89

Qy   61 CCTGCTCCAGGCCCTCACTGTGCAAACTGCTGTGTCCACTGCCTTCTGTCTGTCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 CCTGCTCCAGGCCCTCACTGTGCAAACTGCTGTGTCCACTGCGTTCTGGTGTCCCAT 149

Qy   121 CCCCAGGAGGTTGCCCCCGGATGCAGGGAGGAGTTCCCCCTTGGGAGGAGGCTCTTCTCTGGGGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 CCCCAGGAGGTTGCCCCCGGATGCAGGGAGGAGTTCCCCCTTGGGAGGAGGCTCTTCTCTGGGGGAA 209

Qy   181 GATGACCCCACTGGGCCGGAGGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGAGGAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   210 GATGACCCCACTGGGCCGGAGGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGAGGAGGAT 269

Qy   241 CCACCCGGAGAGGAGGATCTACCTGAGAGGAGGAGCTACTTGAGAGGAGGATCTACCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   270 CCACCCGGAGAGGAGGATCTACCTGAGAGGAGGAGCTACCTGAGAGGAGGATCTACCT 329

Qy   301 GAAAGTTAAGCCTAAATCAGGAAGAAGGAGGATCTCCCTGAAGTTTAGAGGATCTACCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   330 GAAAGTTAAGCCTAAATCAGAAGAAGGAGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 389

Qy   361 GAGGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATTGCCCACAGGGCAAAAGAAAGAGGAGGAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   390 GAGGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAAGAGGAGGAT 449

LOCUS   AL554705   1070 bp   mRNA   linear   EST 30-MAR-2004
DEFINITION   AL554705 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
             clone CS0DI085YF18 5-PRIME, mRNA sequence.
ACCESSION   AL554705
VERSION   AL554705.3 GI:45859455

ORIGIN

Query Match   41.7%; Score 635; DB 1; Length 927;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 685; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   18 TCCCCTGTGCCCCAGCCCTGGCTCCCTCTGGTTGATCCCCGGCCCCTGCTCCAGGCCCTCAC 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   36 TCCCCTGTGCCCCAGCCCTGGCTCCCTCTGGTTGATCCCCGGCCCCTGCTCCAGGCCCTCAC 95

Qy   78 TGTGCAAACTGCTGTGTCCACTGCCTTCTGTCTGTCCATCCCCAGGAGGTTGCCCCG 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 TGTGCAAACTGCTGTGTCCACTGCGTTCTGGTGTCCATCCCCAGGAGGTTGCCCCG 155

Qy   138 GATGCAGGGAGGAGTTCCCCCTTGGGAGGAGGCTCTTCTCTGGGGGAAGACCCACTGGGCCGGA 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   156 GATGCAGGGAGGAGTTCCCCCTTGGGAGGAGGCTCTTCTCTGGGGGAAGATGACCCACTGGGCCGGA 215

Qy   198 GGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGAGGAGGAGGA 257
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 GGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGAGGAGGAGGA 275

Qy   258 TCTACCTGGAGAGGAGGATCTACCTGAGAGGAGGATCTACCTGAAAGTTAAGCCTAAATC 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 TCTACCTGGAGAGGAGGATCTACCTGAGAGGAGGATCTACCTGAAAGTTAAGCCTAAATC 335

Qy   318 AGAAGAAGGAGGGCTCCCTGAAGTTAGAGGATCTACCTGTTGAGGGCTCCTGGAGATCC 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336 AGAAGAAGGAGGGCTCCCTGAAGTTAGAGGATCTACCTGTTGAGGGCTCCTGGAGATCC 395

Qy   378 TCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAAGAGGAGGAGTCATTGGGCG 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   396 TCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAAGAGGAGGAGTCATTGGGCG 455

Qy   438 CTATGGAGGGGACCACCGGCCGCCTCGGCCGCGGTGTCCCAGCCTCGCGCCGCTTCCAGTC 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   456 CTATGGAGGGGACCACCGGCCGCCTCGGCCGCGGTGTCCCAGCCTCGCGCCGCTTCCAGTC 515

Qy   498 CCCGGTGGGATATTCCGCGCCCCAGCCTCGCGCGCCCCGGGGTGTCCCAGCCGCCCCCTGGAACT 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   516 CCCGGTGGGATATCCGCGCCCCAGCCTCGCGCGCCCCGGGGTGTCCCAGCCGCCCCCTGGAACT 575

Qy   558 CCTGGGGCTTCCAGCTCCCGCGCCTCCCAGAGAGACTGCGCGCTGGCGCAACAATGGGCCACAGTGT 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   576 CCTGGGGCTTCCAGCTCCCGCGCCTCCCAGAGAACTGCGCGCTGGCCAACAATGGGCCACAGTGT 635

Qy   618 GCAACTGACCCCTGCCTCTGGGCTAGAGATGGCTCTCGGGTGGCTAGTACCCGGGC 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   636 GCAACTGACCCCTGCCTCTGGGCTAGAGATGGCTCTCGGGTCCCGGGAGTACCCGGGC 695

Qy   678 TCTGCAGCTGCATCTCGACTGGGGGGG 703
              ||||||||||||||||||||||||||||
Db   696 TCTGCAGCTGCATCTGCACTGGGGGGG 721

2

RESULT 10
BG386425
LOCUS   BG386425   874 bp   mRNA   linear   EST 12-MAR-2001
DEFINITION 6024556S2F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583869 5',
            mRNA sequence.
ACCESSION   BG386425
VERSION   BG386425.1 GI:13279871
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 874)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: NIH Intramural Sequencing Center
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1308 row: h column: 14
            High quality sequence stop: 714.

FEATURES   Location/Qualifiers
     source   1..874
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4583869"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_15"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     and Supercript II RT (Life Technologies)"

ORIGIN

Query Match   40.5%; Score 617; DB 4; Length 874;
Best Local Similarity   100.0%; Pred. No. 3.7e-305;
Matches   617; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   207 GCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAGGAGGATCCACCCGGAGGAGGAGGAGGA 266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   207 GCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAGGAGGATCCACCCGGAGGAGGAGGAGGA 266

Qy   421 GACCAGAGTCATTGGCGCTATGGAGGAGGCCAGACCCCCGGGGTGTCCCCAGCCCTGC 480
          ||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Db   450 GACCAGAGTCATTGGCGCTATGGAGGAGGCCGACCCCTGGCGTGTCCCCAGCCCTGC 509

Qy   481 GCGGGCGCCGCCTTCCAGTCCCCGGGTGGATATTCCGCCCCCAGCTCGCCGCCTTCTCTGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   510 GCGGGCGCCGCCTTCCAGTCCCCGGGTGGATATTCCGCCCCCAGCTCGCCGCCTTCTCTGC 569

Qy   541 CTGCGCGCCCCCTGGGAACTCCAGCTCCGGCTTCCCAGAACTGCGCGCCTGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   570 CTGCGCGCCCCCTGGGAACTCCAGCTCCGGCTTCCCAGAACTGCGCGCCTGCC 629

Qy   601 AACAATGGCCACAGTGTGTCCCCCTGCCTCCTCGGGGCCCCTGGGCCCTGGG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   630 AACAATGGCCACAGTGCGAACTGACCCCTCCCTGGGCTAGAGATGGCTCTGGGGTCCC 689

Qy   661 GGGCGCGGAGT 670
          |||||||||||
Db   690 GGGCGCGGAGT 699

RESULT 11
AI925646/c
LOCUS   AI925646   669 bp   mRNA   linear   EST 08-MAR-2000
DEFINITION wo32d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457037 3'
            similar to TR:Q16790 Q16790 CARBONIC ANHYDRASE ;, mRNA sequence.
ACCESSION   AI925646
VERSION   AI925646.1 GI:5661536
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 669)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D. & Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Insert Length: 819   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 416.

Db   1 GCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAGGAGGATCCACCCGGAGGAGGAGGAGGA 60

Qy   267 AGAGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCTGGAGTTAAGCCTAAATCAGAAGAAGGAAGA 326

Db   61 AGAGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCTGGAGTTAAGCCTAAATCAGAAGAAGGAAGA 120

Qy   327 GGGGCTCCCTGAAGGTTAGAGGGATCTACCTACTGTTGAGGGTCCTGGAGATCCTCAAGAACC 386

Db   121 GGGGCTCCCTGAAGGTTAGAGGGATCTACCTACTGTTGAGGGTCCTGGAGATCCTCAAGAACC 180

Qy   387 CCAGAATAATTGCCCACAGGGACAAAGAAGGGGATGACCAGAGTCATTGGGGCTATGGGAG 446

Db   181 CCAGAATAATTGCCCACAGGGACAAAGAAGGGGATGACCAGAGTCATTGGGGCTATGGGAG 240

Qy   447 CGACCCGCGCCTGGCCCGGGAGTGTCCCCAGCCCTGCGCGGGCGCTTCCCAGTCCCCGGTGGA 506

Db   241 CGACCCGCGCCTGGCCCGGGAGTGTCCCCAGCCCTGCGCGGGCGCTTCCCAGTCCCCGGTGGA 300

Qy   507 TATCCGCCCCCAGCTCGCGCGCCTTCTCTGCCTGCGCGCCCCCTGGGGAACTCCTGGGCTT 566

Db   301 TATCCGCCCCCAGCTCGCGCGCCTTCTCTGCCTGCGCGCCCCCTGGGGAACTCCTGGGCTT 360

Qy   567 CCAGCTCCGGCTTCCCAGAACTGCGCGCCTCCCAGAACAATGGCCACAGTGTGCAACTGAC 626

Db   361 CCAGCTCCGGCTTCCCAGAACTGCGCGCCTCCCAGAACAATGGCCACAGTGTGCAACTGAC 420

Qy   627 CCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCCGGGCGCGGAGACCACACTGTGAAGCT 686

Db   421 CCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCCGGGCGCGGAGACCACACTGTGAAGCT 480

Qy   687 GCATCTGCACTGGGGGGGCGTGCAGTGTCGTCTCCGGGGTCGGAGCCACCGGGAGCCACCG 746

Db   481 GCATCTGCACTGGGGGGGCGTGCAGTGTCGTCTCCGGGGTCGGAGCCACCGGGAGCCACCG 540

Qy   747 TTTCCCTGCCGGAGATCCACGTGGTTCACCTCAGCACCGCCCTTTGCCAGGTTGACGAGGC 806

Db   541 TTTCCCTGCCGGAGATCCACGTGGTTCACCTCAGCACCGCCCTTTGCCAGGTTGACGAGGC 600

Qy   807 CTTGGGGGCGCCCGGGAG 823

Db   601 CTTGGGGGCGCCCGGGAG 617

RESULT 12

```
CA429535/c
LOCUS       CA425935              689 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-FE1-beg-j-10-0-UI.s1 NCI_CGAP_FE1 Homo sapiens cDNA clone
            UI-H-FE1-beg-j-10-0-UI 3', mRNA sequence.
ACCESSION   CA425935
VERSION     CA425935.1  GI:24788661
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 689)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            The following repetitive elements were found in this cDNA
            sequence: 1-42, >AT_rich#low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            PolyA=Yes.
FEATURES             Location/Qualifiers
     source          1..689
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FE1-beg-j-10-0-UI"
                     /tissue_type="Cell lines"
                     /clone_lib="NCI_CGAP_FE1"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FE1 is a normalized cDNA library
                     derived from a pool of mRNA obtained from 3 cell lines
                     from grade II chondrosarcoma tissues. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCTACGGAC. The cell lines were provided by Dr James
                     Martin from the University of Iowa.
                     TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
                     TAG_LIB=UI-H-FE1
                     TAG_SEQ=CGCTACGGAC"
ORIGIN
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Query Match   36.5%;   Score 555;   DB 6;   Length 689;
Best Local Similarity 99.7%;   Pred. No. 2.7e-273;
Matches 655; Conservative   0;   Mismatches 2;   Indels 0;   Gaps 0;

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Qy    849 GGAGGAGGGGCCCCGAAGAAAACAGTGCCTATGAGCAGTTGCCTGTCTCCGCTTGGAGAAAT 908
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Db    689 GGAGGAGGGGCCCCGAAGAAAACAGTGCCTATGAGCAGTTGCCTGTCTCCGCTTGGAGAAAT 630

Qy    909 CGCTGAGGAAGGGCTCAGAGACTCAGGGTCCCAGAGACTGGACATATCTGACTCCTGCCCTC 968
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    629 CGCTGAGGAAGGGCTCAGAGACTCAGGGTCNCAGAGACTGGACATATCTGACTCCTGCCCTC 570

Qy    969 TGACTTCAGCCGTACTTCCAATATGAGGGGGTCTCGACTACACCGGCCCCTGTGCCCAGGG 1028
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Db    569 TGACTTCAGCCGCTACTTCCGATATGAGGGGGTCTCTGACTACACCGGCCCCTGTGCCCAGGG 510

Qy   1029 TGTCATCTGGACTGTGTTTAACCAGACAGAGTGATCTGAGTGCTAAGCAGCTCCACACCCT 1088
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Db    509 TGTCATCTGGACTGTGTTTAACCAGACAGAGTGATCTGAGTGCTAAGCAGCTCCACACCCT 450

Qy   1089 CTCTGACACCCTGTGGGGGACCTGGTGACTTCGGGCTACAGCTGAACTTCCGAGCGACGCA 1148
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Left column (rotated):

FEATURES   Location/Qualifiers
     source   1..669
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:2457037"
                  /tissue_type="poorly differentiated adenocarcinoma with
                  signet ring cell features"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_Gas4"
                  /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                  Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.69 kb. Life Technologies catalog #:
                  11549-011"
ORIGIN

Query Match   36.5%;   Score 555;   DB 1;   Length 669;
Best Local Similarity 99.8%;   Pred. No. 2.7e-273;
Matches 605; Conservative   0;   Mismatches 1;   Indels 0;   Gaps 0;

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Qy    917 AAGGCTCAGAGACTCAGGTCCCAGGACTGGGACATATCTGACTCCTGCCCTCTGACTTCA 976
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Db    606 AAGGCTCAGAGACTCAGGTCCCAGGACTGGGACATATCTGACTCCTGCCCTCTGACTTCA 547

Qy    977 GCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGGCCCCTGTGCCCAGGGTGTCATCT 1036
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 GCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGGCCCCTGTGCNCAGGGTGTCATCT 487

Qy   1037 GGACTGTGTTTAACCAGACAGAGTGATGTCTGAGTGCTAAGCAGCAGTCCACACCCTCTCTGACA 1096
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Db    486 GGACTGTGTTTAACCAGACAGAGTGATGCTAAGCAGCAGTCCACACCCTCTCTGACA 427

Qy   1097 CCCTGTGGGGGACCTGGTGACTCTGGGCGCTACAGCTTCCGAGCGACGACGCAGCCTTTGA 1156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 CCCTGTGGGGGACCTGGTGACTCTGGGCTACAGCTTCCGAGCGACGACGCAGCCTTTGA 367

Qy   1157 ATGGGGCGAGTGAGTTGAGGGCCTCCTTCCCTGTCCCTGGAGTGGACAGCAGTCCTCGGGTCTGCTG 1216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 ATGGGGCGAGTGAGTTGAGGGCCTCCTTCCCTGTCCCTGGAGTGGACAGCAGTCCTCGGGTCTGCTG 307

Qy   1217 AGCCAGTCCAGCTGAATTCCTGCCTCCCTGGCTGCTGCGGTGACATTCCTTAGCCCTGGTTTTTGGCC 1276
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Db    306 AGCCAGTCCAGCTGAATTCCTGCCTCCCTGGCTGCTGCGGTGACATCCTTAGCCCTGGTTTTTGGCC 247

Qy   1277 TCCTTTTTGCTGTCACCAGCGGTCGGCGGTTCCTGTGTGCAGATGAGAAGGCAGCACAGAAGGG 1336
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Db    246 TCCTTTTTGCTGTCACCAGCGTCGGCGGTTCCTGTGTGCAGATGAGAAGGCAGCACAGAAGGG 187

Qy   1337 GAACCAAAGGGGGTGTAGACTACCGCCCAGCAGAGGTTAGCCCAGAGCTAGAGGC 1396
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Db    186 GAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTTAGCCCAGAGCTAGAGGC 127

Qy   1397 TGGATCTTGGAGNAATGTGAGAAGCCAGCCAGCGACGAGGGCATCTGACGGGGACCGGGTAACTGTC 1456
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Db    126 TGGATCTTGGAGAATGTGAGAAGCCAGCCAGCCATCTGAGGGGGGACCGGGTAACTGTC 67

Qy   1457 CTGTCCTGCTCATTATTGCCACTTCCTTTCCTTTAACTGCCAAGAAAATTTTTTAAAATAAAATATT 1516
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Db     66 CTGTCCTGCTCATTATTGCCACTTCCTTTCCTTTAACTGCCAAGAAATTTTTTAAAATAAAATATT 7

Qy   1517 TATAAT 1522
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Db      6 TATAAT 1
```

RESULT 13

```
LOCUS       BM552941                 627 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6542619 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742739
            5', mRNA sequence.
ACCESSION   BM552941
VERSION     BM552941.1  GI:18791234
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 627)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12761 row: f column: 20
            High quality sequence stop: 599.
FEATURES             Location/Qualifiers
     source          1..627
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5742739"
                     /tissue_type="medulla"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_119"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: EcoRV (destroyed); RNA source normal medulla from
                     anonymous male age 27. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.3 kb, insert size range
                     0.9-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 013. Note:
                     this is a NIH_MGC Library."
```

Alignment (RESULT 13):

```
Db    449  CTCTGGACACCCTGTGGGGACCTGGTGGACCTCGGCTACCAAGCTGAACTTCCGACGCGACCCA  390
Qy   1149  GCCTTTGAATGGGCCGGAGTGATTGAGGGCCTTCCTTCCTTGGGACTGGACAGCAGTCCTCG   1208
Db    389  GCCTTTGAATGGGCCAGTGATTGAGGGCCTTCCTTCCTGCTGGACAGCAGTCCTCG        330
Qy   1209  GGCTGGCTGAGCCAGTCCAGCTGAATTCCTGCGTGCTGGTGGACATCCTAGCCCTGGT     1268
Db    329  GGCTGGCTGAGCCAGTCCAGCTGAATTCTGCGTGCTGGTGGACATCCTAGCCCTGGT       270
Qy   1269  TTTGGGCCTCCTTTTTGCTGTGTCACCAGCGGTCGCGGTTCCTTGGTGCAGATGAGGAAGGCAGCA  1328
Db    269  TTTTGGGCCTCCTTTTTGCTGTGTCACCAGCGGTCGCGGTTCCTTGGTGCAGATGAGGAAGGCAGCA 210
Qy   1329  CAGAAGGGGGAACCAAAAGGGGGTGTGAGCTACCAGCTGGAGAGTGACTGGAGC          1388
Db    209  CAGAAGGGGGAACCAAAAGGGGGTGTGAGCTACCAGCTGGAGAGTGACTGGAGC          150
Qy   1389  CTAGAGGGGCTGGGATCTTGGAGAAGTGTGAGGAAGCCAGCAGCCAGCATCTGAGGGGGGAGCCGG 1448
Db    149  CTAGAGGGGCTGGGATCTTGGAGAAGTGTGAGGAAGCCAGCAGCCAGCATCTGAGGGGGGAGCCGG  90
Qy   1449  TAACTGTCCTGTCCTGCTCATTATCCCACTTCCTTTTAACTGCCAAGAAAATTTTTTA       1505
Db     89  TAACTGTCCTGTCCTGCTCATTATGCCCACTTCCTTTTAACTGCCAAGAAAATTTTTTTA  33
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RESULT 14

```
ORIGIN
            Query Match      34.9%;  Score 531;  DB 4;  Length 627;
            Best Local Similarity   100.0%;  Pred. No. 5.9e-261;
            Matches  531;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    990  ATATGAGGGGGTCTCGACTACACCCGCCCCTGTGCCCAGGGGTGTCATGTGGACTGTGTTTAA  1049
Db     52  ATATGAGGGGTTCTCTGACTACACCCGCCCCTGTGCCCAGGGGTGTCATGTGGACTGTGTTAA  111
Qy   1050  CCAGACAGTGATTGCTGAGTGGTAAGGAGCTCCACACCCTTTCTCGACACCCTGTGTGGGGACC  1109
Db    112  CCAGACAGTGATGCTGAGTGGTAAGGAGCTCCACACCCTTTCTCGACACCCTGTGTGGGGACC  171
Qy   1110  TGGTGACTCTCGGGCTACAGCTGAACTTCCGAGGCGACGGACAGCCGCCTTTGAAATGGGCG   1169
Db    172  TGGTGACTCTCGGGCTACAGCTGAACTTCCGAGGCGACGGACAGCCGCCTTTGAAATGGGCG   231
Qy   1170  TGAGGGCCTCCTTCCTTGCTGGACACACAGCTGCTCTGGGGGCTCCAGCAGTCCAGCT      1229
Db    232  TGAGGGCCTCCTTCCTTGCTGGACACACAGCTGCTCTGGGGGCTCCAGCAGTCCAGCT      291
Qy   1230  GAATTCCTGCCTGGCTGGCTGGACATCTTAGCCCTGGTTTTGGGCCTCCTTTTTGCTGT     1289
Db    292  GAATTCCTGCCTGGCTGGCTGGACATCTTAGCCCTGGTTTTGGGCCTCCTTTTTGCTGT     351
Qy   1290  CACCAGCGTCGCGGTTCCTTGGTGCAGATGAGGAAGGCAGCACAGAAGGGGGAACCAAAAGGGGG  1349
Db    352  CACCAGCGTCGCGGTTCCTTGGTGCAGATGAGGAAGGCAGCACAGAAGGGGGAACCAAAAGGGGG  411
Qy   1350  TGTGAGCTACCGGCCCAGCCAGAGGTAGCCGAGACTGGAGCCTTAGAGGCTGGATCTTGGAGA  1409
Db    412  TGTGAGCTACCGGCCCAGCCAGAGGTAGCCGAGACTGGAGCCTTAGAGGCTGGATCTTGGAGA  471
Qy   1410  ATGTTGAGGAAGCCAGCCAGAGGCAGCCATCTGAGGGGGGAGCCGGTAACTGTCCTGTCCTGCTCAT  1469
Db    472  ATGTTGAGGAAGCCAGCCAGAGGCAGCCATCTGAGGGGGGAGCCGGTAACTGTCCTGTCCTGCTCAT  531
Qy   1470  TATGCCACTTCCTTTTAACTGCCAAGAAAATTTTTTTAAAATAAAATATTTATA          1520
Db    532  TATGCCACTTCCTTTTAACTGCCAAGAAAATTTTTTTAAAATAAAATATTTATA          582
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```
LOCUS       CA416326/c
LOCUS       CA416326                 659 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-FE0-bbu-i-22-0-UI.s1 NCI_CGAP_FE0 Homo sapiens cDNA clone
            UI-H-FE0-bbu-i-22-0-UI 3', mRNA sequence.
ACCESSION   CA416326
VERSION     CA416326.1  GI:24778977
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 659)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            The following repetitive elements were found in this cDNA
            sequence: 1-42, >AT rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
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RESULT 15

LOCUS   AI831707   682 bp   mRNA   linear   EST 21-DEC-1999
DEFINITION wj40h01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2405329 3'
            similar to TR:Q16790 Q16790 CARBONIC ANHYDRASE ;, mRNA sequence.
ACCESSION   AI831707
VERSION   AI831707.1 GI:5452464
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 682)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1322   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 424.
FEATURES   Location/Qualifiers
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                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2405329"
                    /tissue_type="squamous cell carcinoma, poorly
                    differentiated (4 pooled tumors, including primary and
                    metastatic)"
                    /dev_stage="adult"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NCI_CGAP_Lu19"
                    /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                    modified polylinker; 1st strand cDNA was primed with a Not I
                    - oligo(dT) primer. Double-stranded cDNA was ligated to
                    Eco RI adaptors (Pharmacia), digested with Not I and
                    cloned into the Not I and Eco RI sites of the modified
                    pT7T3 vector. Library went through one round of
                    normalization. Library constructed by Bento Soares and M.
                    Fatima Bonaldo. "

ORIGIN

Query Match   33.8%; Score 514; DB 1; Length 682;
Best Local Similarity 99.7%;
Matches   514; Conservative   0; Mismatches   2; Indels   0; Gaps   0;
                                    Pred. No. 3.2e-252;

Qy   907 ATCGGCTGAGGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACACATATCTGCACTCCTGCC 966
          ||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   616 ATCGGCTGAGGAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTCCTGCCTGCCT 557

Qy   967 TCTGACTTCAGCGCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCCGCCCGTGCCCAG 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556 TCTGACTTCAGCGCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCCGCCCGTGCCCAG 497

Qy   1027 GGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGGTAAGCAGCTCCACAGC 1086
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 GGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGGNAAGCAGCTCCACACC 437

Qy   1087 CTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACG 1146
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Db   436 CTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACG 377

Qy   1147 CAGCCTTTGAATGGGCGAGTGATTGAGGCGCTCCTTCCCTGCTCGGACGTGGACCAGCAGTCCT 1206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 CAGCCTTTGAATGGGCGAGTGATTGAGGCGCTCCTTCCCTGCTCGGACGTGGACCAGCAGTCCT 317

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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="UI-H-FE0-bbu-i-22-0-UI"
            /dev_stage="Adult"
            /tissue_type="Chondrosarcoma Cell line"
            /lab_host="DH10B (Life Technologies)"
            /clone_lib="NCI_CGAP_FE0"
            /note="Vector: pT7T3-Pac (Pharmacia) with a modified
            polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FE0 is
            a cDNA library containing the following tissue(s): a pool
            of 3 chondrosarcoma cell lines (grade 2) The library was
            constructed according to Bonaldo, Lennon and Soares,
            Genome Research, 6:791-806, 1996. First strand cDNA
            synthesis was primed with an oligo-dT primer containing a
            Not I site. Double stranded cDNA was ligated to an EcoR I
            adaptor, digested with Not I, and cloned directionally
            into pT7T3-Pac vector. The oligonucleotide used to prime
            the synthesis of first-strand cDNA contains a library tag
            sequence that is located between the Not I site and the
            (dT)18 tail. The sequence tag for this library is
            CGCTACGGAC. The cell lines was provided by Dr James Martin
            of University of Iowa.
            TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
            TAG_LIB=UI-H-FE0
            TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match   34.6%; Score 526; DB 6; Length 659;
Best Local Similarity 100.0%;
Matches   526; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
                                    Pred. No. 2.2e-258;

Qy   997 GGGTCTCTGACTACACCCGCCCTGTGCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACA 1056
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Db   541 GGGGTCTCTGACTACACCCGCCCTGTGCCCAGGGTGTCATCTGACTGTGTTTAACCAGACA 482

Qy   1057 GTGATGCTGAGTGGTAAGCAGCTCCACACCCTCTCTGACACCCTGTGGGGACCTGGTGAC 1116
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGATGCTGAGTGGTAAGCAGCTCCACACCCTCTCTGACACCCTGTGGGGACCTGGTGAC 422

Qy   1117 TCTCGGCTACAGCTGAACTTCCGAGCGCAGCAGCCTTTGAATGGGCGAGTGATTGAGCGC 1176
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCTCGGCTACAGCTGAACTTCCGAGCGCAGCAGCCTTTGAATGGGCGAGTGATTGAGCGC 362

Qy   1177 TCCTTCCCTGCTCGGACGGACAGTCCTCCTCCGGGCTGCTGAGCCAGTCCAGCTGAATTCC 1236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCCTTCCCTGCTCGGACGGACAGTCCTCCTCCGGGCTGCTGAGCCAGTCCAGCTGAATTCC 302

Qy   1237 TGGCCTGGCGGCTGCTGGTGACATCCTAGCCCTGTCCTTTTTTGGCCTGTCGTCACCAGC 1296
          || |||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   301 TGCCTGGCGTGCTGGTGACATCCTAGCCCTGTCCTTTTTGCCCTGTCGTCACCAGC 242

Qy   1297 GTGCGGCGGTTCCTTGTGTGCAGATGAGGAGGCAGCACAGAAGGGGACCAAAAGGGGTGTGAGC 1356
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   241 GTGCGGCGGTTCCTTGTGCAGATGAGGAGGCACAGAAGGGGACCAAAAGGGGTGTGAGC 182

Qy   1357 TACCGCGCCAGCGAGGTAGCCCAGAGCTGGGCTGGGCTTGGAGAAGTGTGAG 1416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TACCGCGCCAGCGAGGTAGCCCAGAGCTGGGCTGGGCTTGGAGAAGTGTGAG 122

Qy   1417 AAGCCAGCCAGCGCATCTGAGGGGGAGCCCGGTTAACTGTTCTGTTCTGCTCTTATTATGCCA 1476
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Db   121 AAGCCAGCCAGCGCATCTGAGGGGGAGCCCGGTTAACTGTTCTGTTCTGCTCTTATTATGCCA 62

Qy   1477 CTTCCTTTTTAACTGCCAAGAAATTTTTTAAATAAATAAATATTTATTAT 1522
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTTCCTTTTTAACTGCCAAGAAATTTTTTAAATAAATAAATATTTATTAT 16

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Qy   1207 CGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCTGGGTGACATCCTAGCCCTG 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    316 CGGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGGGTGACATCCTAGCCCCTG 257

Qy   1267 GTTTTTGGCCTCCTCTTTTTGCTGTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAAGGCAG 1326
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1327 CACAGAAGGGGGAACCAAAGGGGTGTGAGCTACCGCCCAGCGAGAGGTAGCCGAGACTGGA 1386
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Qy   1387 GCCTAGAGGCTGGATCTTGGGAGAATGTGAGAAGCCAGCAGAGGCCATCTGAGGGGGGAGCC 1446
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Db    136 GCCTAGAGGCTGGATCTTGGGAGAATGTGAGAAGCCAGCAGAGGCCATCTGAGGGGGGAGCC 77

Qy   1447 GGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAAATTTTTAA 1506
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     76 GGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAAATTTTTTAA 17

Qy   1507 AATAAAATATTTATAAT 1522
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Search completed: February 6, 2005, 10:50:07
Job time : 4455 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: February 5, 2005, 23:23:52 ; Search time 6352 Seconds
(without alignments)
11331.065 Million cell updates/sec

Title: US-09-967-237A-1
Perfect score: 1522
Sequence: 1 acagtcagccgccatggcccc..........ttaaaataaatattattataat 1522
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4526729 seqs, 2364849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1522	100.0	1522	6	AR074439	AR074439 Sequence
2	1522	100.0	1522	6	AR081119	AR081119 Sequence
3	1522	100.0	1522	6	AR085316	AR085316 Sequence
4	1522	100.0	1522	6	AR088064	AR088064 Sequence
5	1522	100.0	1522	6	AR104223	AR104223 Sequence
6	1522	100.0	1522	6	AR143487	AR143487 Sequence
7	1522	100.0	1522	6	AR171392	AR171392 Sequence
8	1522	100.0	1522	6	AR171563	AR171563 Sequence
9	1522	100.0	1522	6	BD243152	BD243152 MN gene a
10	1522	100.0	1552	6	CQ834035	CQ834035 Sequence
11	1522	100.0	1552	6	AX330007	AX330007 Sequence
12	1522	100.0	1552	6	AX332607	AX332607 Sequence
13	1522	100.0	1552	6	AX333244	AX333244 Sequence
14	1522	100.0	1552	6	AX336174	AX336174 Sequence
15	1522	100.0	1552	9	X66839	X66839 H.sapiens M
16	1520.4	100.0	1639	9	BC014950	BC014950 Homo sapi
17	1517.4	99.7	1519	9	AJ010588	AJ010588 Homo sapi
18	1399	91.9	1399	6	AR095263	AR095263 Sequence
19	1247.4	82.0	1289	6	CQ726696	CQ726696 Sequence
20	759.2	49.9	1965	10	MMU245857	AJ245857 Mus muscu
21	457.8	30.1	1671	10	AB086322	AB086322 Mus muscu
22	414.4	27.2	6521	6	CQ806582	CQ806582 Sequence
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24	414.4	27.2	6521	6	AX821141	AX821141 Sequence
25	414.4	27.2	6521	6	AX825781	AX825781 Sequence
26	414.4	27.2	10898	6	AR074442	AR074442 Sequence
27	414.4	27.2	10898	6	AR081122	AR081122 Sequence
28	414.4	27.2	10898	6	AR085319	AR085319 Sequence
29	414.4	27.2	10898	6	AR088067	AR088067 Sequence
30	414.4	27.2	10898	6	AR104226	AR104226 Sequence
31	414.4	27.2	10898	6	AR143490	AR143490 Sequence
32	414.4	27.2	10898	6	AR171395	AR171395 Sequence
33	414.4	27.2	10898	6	AR171566	AR171566 Sequence
34	414.4	27.2	187856	9	BD243155	BD243155 MN gene a
35	414.4	27.2	88328	9	AL357874	AL357874 Human DNA
36	414.4	27.2	415	6	AF334829	AF334829 Homo sapi
37	413.4	27.2	415	6	AR074454	AR074454 Sequence
38	413.4	27.2	415	6	AR081134	AR081134 Sequence
39	413.4	27.2	415	6	AR085331	AR085331 Sequence
40	413.4	27.2	415	6	AR088079	AR088079 Sequence
41	413.4	27.2	415	6	AR104238	AR104238 Sequence
42	413.4	27.2	445	6	AR143502	AR143502 Sequence
43	413.4	27.2	445	6	AR171406	AR171406 Sequence
44	413.4	27.2	445	6	AR171577	AR171577 Sequence
45	413.4	27.2	445	6	BD243167	BD243167 MN gene a

ALIGNMENTS

RESULT 1
AR074439

LOCUS   AR074439   1522 bp   DNA   linear   PAT 28-AUG-2000
DEFINITION Sequence 1 from patent US 5955075.
ACCESSION   AR074439
VERSION   AR074439.1 GI:10001194
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 1 21-SEP-1999;
FEATURES   Location/Qualifiers
     source   1..1522
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ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 ACAGTCAGCCGCCATGGCTCCCCGTGCCCCAGCCCCGTGGCGTCCTCGTTGTGATCCCGCC 60

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Qy   361 GAGGCTCCTGGAGATCCTTCAAGAACCCCAGAATAAATGCCCACAGG 420
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Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCGGAGTGTCCCAGC 480
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Qy   841 GCCTTTCTGGGAGGAAGGGCCCGGAAGAAAACAGTGCCTATGAGCAG 900
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Qy   901 GAAGAAAATCGCTGAGGAAGGGCTCAGGTCCCAGGACTCAGTCCCA 960
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RESULT 2

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LOCUS       AR081119                1522 bp    DNA    linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5972353.
ACCESSION   AR081119
VERSION     AR081119.1    GI:10007847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1..1522
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Query Match             100.0%;  Score 1522;  DB 6;  Length 1522;
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Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy    61 CCTGCTCCAGGCCTCACTGTGCAAACTGCTCTGCGTGTCACTGCTGCTTCCGA 120
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Qy   181 GATGACCCACTGGGCGAGGAGGATTCTGCCCAGTGAAGAGGATTCACCCAGCC 240
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RESULT 3
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LOCUS       AR085316               1522 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 1 from patent US 5981711.
ACCESSION   AR085316
VERSION     AR085316.1  GI:10012085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J.; Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 1 09-NOV-1999;
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FEATURES             Location/Qualifiers
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Query Match   100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity   100.0%;   Pred. No. 1.6e-310;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Sequence 1 from patent US 5989838.
ACCESSION   AR088064
VERSION     AR088064.1  GI:1001427
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 1 23-NOV-1999;
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Best Local Similarity   100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       121 CCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTCGGGGAA    180
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Db       181 GATGAGCCACTGGGCGGAGGAGATCTGCCCAGTGAAGAGGATTCACCCAGAGGCTC    240

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Qy       301 GAAGTTAAGCCTAAATCAGAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT  360
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Db       301 GAAGTTAAGCCTAAATCAGAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT  360

Qy       361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAATAAATGCCACAGGGACAAAAGAGGAT  420
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Db       361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAATAAATGCCACAGGGACAAAAGAGGAT  420

Qy       421 GACCAGAGTCATTGGGCGCTATGGAGGGCACCCCACCACCCCACAGCTGC    480
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Qy       481 GCGGGCCGCTTCCAGTCCCCGTGGGAATATCCGCCCGGCCGGGTGCCCGGCC   540
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Qy       541 CTGCGGCCCCTGAACTCTGGGCCTTCCAGCTTCCAGGGTCCCCAGAACTGCGGC   600
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Qy       601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCCTGGGCTCGGGTCCC   660
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Qy       661 GGGCGGGAGGTACCGGGCTCTGCAGCTCGCATCGCCACTGGGGGCGCAGGTCGTCCGGC   720
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Db       661 GGGCGGGAGGTACCGGGCTCTGCAGCTCGCATCGCCACTGGGGGCGCAGGTCGTCCGGC   720

Qy       721 TCGGAGGCACACTGTGGAAGGGCCACCGGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  780
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Qy      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGTAAGCAGCTC  1080
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Db      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGTAAGCAGCTC  1080
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RESULT 5
LOCUS       AR104223                1522 bp    DNA       linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6093548.
ACCESSION   AR104223
VERSION     AR104223.1  GI:12816931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 1 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1..1522
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ORIGIN

Query Match      100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity   100.0%;  Pred. No. 1.6e-310;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy   1 ACAGTCAGCGCGCATGGCTCCCGTGTGCCCCAGCCCGCCGCTCCCTCCCTGTTCGATCCCGGCC 60
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Db   1 ACAGTCAGCGCGCATGGCTCCCGTGTGCCCCAGCCCGCCGCTCCCTCCCTGTTCGATCCCGGCC 60

Qy   61 CCTGCTCTCCAGGCCTCACTGTCCAACTGTCGTGTCACGCCCTGGCCTCCTCTGTTGATCCCAT 120
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Db   61 CCTGCTCTCCAGGCCTCACTGTCCAACTGTCGTGTCACGCCCTGGCCTCCTCTGTTGATCCCAT 120

Qy 121 CCCCAGAGGTTGCCCCCGGATGCAGGAGGATTCACCCAGGCTCTTCTTCTGGGGAA 180
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Db 721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCGGGATCCACTGGGGGCTGGTTCACCTCAGC 780

Qy 781 ACCGGCCTTTGCCCAGAGTTGACGGCCCTTGGGGCCCCGGAGATCCAGGTGTTGGCC 840
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Db 781 ACCGGCCTTTGCCCAGAGTTGACGGCCCTTGGGGCCCCGGAGATCCAGGTGTTGGCC 840

Qy 841 GCCTTTCTCGGAGGAGGGCCCGGAGAAAACAGTGCCTATGAGCAGTTGCGTCTCGCTTG 900
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RESULT 6

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LOCUS       AR143487                1522 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6204370.
ACCESSION   AR143487
VERSION     AR143487.1  GI:15104773
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J. Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 1 20-MAR-2001;
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match             100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity   100.0%;  Pred. No. 1.6e-310;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy          1 ACAGTCAGCGCAATGGCTCCCCTGTGCCCCAGCCCTCCCTCTGTTGATCCCGGCC 60
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Qy         61 CCTGCTCCAGGGCCTCACTGTGCAACTGTCTGCTTCTCTGATGCCTGTCCAT 120
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Qy       1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGAGAGGCATCTGAGGG 1440
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LOCUS   AR171392   1522 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION   Sequence 1 from patent US 6297041.
ACCESSION   AR171392
VERSION   AR171392.1 GI:17910342
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   MN gene and protein
  JOURNAL   Patent: US 6297041-A 1 02-OCT-2001;
FEATURES   Location/Qualifiers
     source   1..1522
                     /organism="unknown"
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ORIGIN

Query Match   100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity   100.0%; Pred. No. 1.6e-310;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    121 CCCCAGAGGTTGCCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTGGGGAA 180
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Db    961 CTGCCCTCTGACTTCAGCCGCCGCTACTTCCAATATGAGGGTTCTGACTACACCGCCCTGT 1020

Qy   1021 GCCCAGGGGGTGTCACTCTGGACTGTGTTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
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Db   1021 GCCCAGGGGGTGTCATCTGGACTGTGTTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080

Qy   1081 CACACCCCTCTCTGACACCCTGTGGGGGAACCTGGTCGACTCTCGGCTACAGTGAACTTCCGA 1140
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Qy   1141 GCGAGCGCAGCCTTTGAAATGGGGAGTGAGTTGATTGAGGGCCTCCTCTCCTTCCCGTGCTGGAGTGGACAGC 1200
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Db   1261 GCCCTGGGTTTTGGCCTCCTTTTTGGCTGCTGTCACCAGGGGTCGCGGTTCCTTGTTGGCAGATGAGA 1320

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Db   1501 TTTTAAAAATAAATATTTATAAT 1522
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RESULT 8
LOCUS   AR171563   1522 bp   DNA   linear   PAT 17-DEC-2001
DEFINITION   Sequence 1 from patent US 6297051.
ACCESSION   AR171563
VERSION   AR171563.1 GI:17910513
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
               Unclassified.
REFERENCE   1 (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE   MN gene and protein
  JOURNAL   Patent: US 6297051-A 1 02-OCT-2001;
FEATURES   Location/Qualifiers

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RESULT 9
BD243152
LOCUS       BD243152                    1522 bp    DNA    linear   PAT 17-JUL-2003
DEFINITION  MN gene and protein.
ACCESSION   BD243152
VERSION     BD243152.1    GI:33052922
KEYWORDS    JP 2002528085-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1522)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 1 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT     Homo sapiens (human)
            PN   JP 2002528085-A/1
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 2000578465
            PR   23-OCT-1998 US 09/177776,23-OCT-1998 US   09/178115 PI
            JAN ZAVADA, SILVIA PASTOREKOVA, JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
            C07K14/47,
            PC   C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02 PC
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FEATURES             Location/Qualifiers
     source          1..1522
                     /organism="Homo sapiens"
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Alignment (left panel):

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source          1..1522
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity  100.0%;  Pred. No. 1,6e-310;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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(DNA sequence alignment rows, Qy/Db, positions 1–1522)

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FEATURES             Location/Qualifiers
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     CDS             (13)..(1389)
     mat_peptide     (124)..(1389).
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ORIGIN
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"

Query Match      100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 ACAGTCAGCCGCANTGGCTCCCCTGTGCCCCGAGCCCCTGGCTCCCCTTGTTGATCCCGGCC 60
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Db       1 ACAGTCAGCCGCANTGGCTCCCCTGTGCCCCGAGCCCCTGGCTCCCCTTGTTGATCCCGGCC 60

Qy      61 CCTGCTCCAGGCCTCACTGTGCAACTGCTCGTTCTGATGCCTGTCCAT 120
Db      61 CCTGCTCCAGGCCTCACTGTGCAACTGCTCGTTCTGATGCCTGTCCAT 120

Qy     121 CCCCAGAGGTTGCCCCGGATGCAGAGGAAGGTTCTTCTGGGGAA 180
Db     121 CCCCAGAGGTTGCCCCGGATGCAGAGGAAGGTTCTTCTGGGGAA 180

Qy     181 GATGACCCACTGGGCGGCGAGGAGGATCAGGAGGATCTGCCCAGTGAAGATCACTACCT 240
Db     181 GATGACCCACTGGGCGGCGAGGAGGATCAGGAGGATCTGCCCAGTGAAGATCACTACCT 240

Qy     241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db     241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Qy     301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCTCGAAGTTAGGAGGATTAGGAGGATCTACTACTGTT 360
Db     301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCTCGAAGTTAGGAGGATTAGGAGGATCTACTACTGTT 360

Qy     361 GAGGCTCCTGGAGATTCCTCAAGAACCCCAGAATAAATGCCCAGGGACAAAAGAAGGGGAT 420
Db     361 GAGGCTCCTGGAGATTCCTCAAGAACCCCAGAATAAATGCCCAGGGACAAAAGAAGGGGAT 420

Qy     421 GACCAGAGTCATTGGGCGTATGGAGGAGGCACCCCGCCCCTGGCCCCCAGCCTGC 480
Db     421 GACCAGAGTCATTGGGCGTATGGAGGAGGCACCCCGCCCCTGGCCCCCAGCCTGC 480

Qy     481 GCGGGGCCGCCTTCCAGTCCCCGGTGGATATCCGGCGTAATCCGGCCCAGCTCCGCGCCTTCTGCCCCGGCC 540
Db     481 GCGGGGCCGCCTTCCAGTCCCCGGTGGATATCCGGCGTAATCCGGCCCAGCTCCGCGCCTTCTGCCCCGGCC 540

Qy     541 CTGCGCCCCCCTGGAACTCCTGGGCTTCAGCTCCCGGCCTTCCAGCTCGCCGCCTTCTGCCCCGGCC 600
Db     541 CTGCGCCCCCCTGGAACTCCTGGGCTTCAGCTCCCGGCCTTCCAGCTCGCCGCCTTCTGCCCCGGCC 600

Qy     601 AACAATGGCCACAGTGTGCAACTGACACCCTGCCTCCTGGGCTTAGAGATGGCTCTGGGGTCC 660
Db     601 AACAATGGCCACAGTGTGCAACTGACACCCTGCCTCCTGGGCTTAGAGATGGCTCTGGGGTCC 660

Qy     661 GGGCGGGAGTACCGGGTGCTCTGCAGCTGCATCGCCCTCCTGGCCTAGAGATGGCTCTGGGGTCC 720
Db     661 GGGCGGGAGTACCGGGTGCTCTGCAGCTGCATCGCCCTCCTGGCCTAGAGATGGCTCTGGGGTCC 720

Qy     721 TCGGAGCACACTGTGGAAGGCACCGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
Db     721 TCGGAGCACACTGTGGAAGGCACCGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780

Qy     781 ACCGGCCTTTGCCAGAGTTGACGACGGCCTTGGGGCGGCCCTGGCCCTCGGGCCTTGGCC 840
Db     781 ACCGGCCTTTGCCAGAGTTGACGACGGCCTTGGGGCGGCCCTGGCCCTCGGGCCTTGGCC 840

Qy     841 GCCTTTCTGGAGGAGGGCCCGGAAGGAAAAACAGTGCCTATGAGCAGTTGCTGCTTCGCTTG 900
Db     841 GCCTTTCTGGAGGAGGGCCCGGAAGGAAAAACAGTGCCTATGAGCAGTTGCTGCTTCGCTTG 900

Qy     901 GAAGAAATCGCTCAGGAGGAGGCTCAGAGACTCAGGTCCCAAGGACTGGACATATCTGCACTC 960
Db     901 GAAGAAATCGCTCAGGAGGAGGCTCAGAGACTCAGGTCCCAAGGACTGGACATATCTGCACTC 960

Qy     961 CTGCCCCTGACTTCAGCGCTACTTCCAAATATGAGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db     961 CTGCCCCTGACTTCAGCGCTACTTCCAAATATGAGAGGGGTCTCTGACTACACCGCCCTGT 1020

Qy    1021 GCCCAGGGGTGTCATCTGGACTGTGTTTTAACCAGACAGAGTAGGGGTCTCGACCAGCTC 1080
Db    1021 GCCCAGGGGTGTCATCTGGACTGTGTTTTAACCAGACAGAGTAGGGGTCTCGACCAGCTC 1080

Qy    1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGGTGTTAACCGAGACAGTGGAACTTCCGA 1140
Db    1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGGTGTTAACCGAGACAGTGGAACTTCCGA 1140

Qy    1141 GCGAGCGCAGGCCTTTGAAATGGGCGAGTGATTGAGGCGGCTCCTTCCCCTGCCCTACCAGC 1200
Db    1141 GCGAGCGCAGGCCTTTGAAATGGGCGAGTGATTGAGGCGGCTCCTTCCCCTGCCCTACCAGC 1200

Qy    1201 AGTCCTCGGGCTGCTGGAGCCCAGTCCAGCTGAAATTCCTCGCTGGGCTGGTGACATCCTA 1260
Db    1201 AGTCCTCGGGCTGCTGGAGCCCAGTCCAGCTGAAATTCCTCGCTGGGCTGGTGACATCCTA 1260

Qy    1261 GCCCTGGGTGTTTTGGCCTCCTTTTGGCTGTCACCAGCGTGGGTGCGGGGTTCCTTGTTGCAGATGAGA 1320
Db    1261 GCCCTGGGTGTTTTGGCCTCCTTTTGGCTGTCACCAGCGTGGGTGCGGGGTTCCTTGTTGCAGATGAGA 1320

Qy    1321 AGGCAGCACAGAAGGGGGACCAAAGGGGTGTGACTACGGCCCAGCACAGAGGTAGCCGAG 1380
Db    1321 AGGCAGCACAGAAGGGGGACCAAAGGGGTGTGACTACGGCCCAGCACAGAGGTAGCCGAG 1380

Qy    1381 ACTGGAGCCTAGAGCGGCTGGATCTTGGAGAATGTGAAGAGCCACCAGCAGGCCATCTGAGGG 1440
Db    1381 ACTGGAGCCTAGAGCGGCTGGATCTTGGAGAATGTGAAGAGCCACCAGCAGGCCATCTGAGGG 1440

Qy    1441 GGAGCCGGGTAACTGTCCTGTCCTGCCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
Db    1441 GGAGCCGGGTAACTGTCCTGTCCTGCCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500

Qy    1501 TTTTAAAATAAAATATTTTATTAT 1522
Db    1501 TTTTAAAATAAAATATTTTATTAT 1522
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RESULT 10
LOCUS            CQ834035              1552 bp    DNA        linear      PAT 29-JUL-2004
DEFINITION       Sequence 71 from Patent EP1439393.
ACCESSION        CQ834035
VERSION          CQ834035.1  GI:50833640
KEYWORDS
SOURCE           Homo sapiens (human)
  ORGANISM       Homo sapiens
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1
  AUTHORS        Astle,J.H., Boardman,L.A., Bugart,L.J., Burgess,C.C., Catino,T.J.,
                 Dwivedi,P., Huntress,M., Johnson,K.A., Lewis,M.E., Maimonis,P.J.,
                 Myerow,S.H., Brown-Shimer,S.L., Thiagalingam,A., Thibodeau,S.N. and
                 Molino,G.A.
  TITLE          Detection methods using TIMP 1 for colon cancer diagnosis
  JOURNAL        Patent: EP 1439393-A 71 21-JUL-2004;
                 Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
                 AND RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1..1552
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match      100.0%;  Score 1522;  DB 6;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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RESULT 11
LOCUS        AX330007                1552 bp    DNA       linear    PAT 09-JAN-2002
DEFINITION   Sequence 516 from Patent WO0194629.
ACCESSION    AX330007
VERSION      AX330007.1  GI:18102985
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
             Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE      Cancer gene determination and therapeutic screening using signature
             gene sets
  JOURNAL    Patent: WO 0194629-A 516 13-DEC-2001;
             Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1..1552
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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Query Match           100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity 100.0%;  Pred. No. 1.6e-310;
Matches 1522; Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;
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Qy   1 ACAGTCAGCGACGCATGGCTCCCCTGCCCAGCCCCTGGCTCTCCGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 ACAGTCAGCGACGCATGGCTCCCCTGCCCAGCCCCTGGCTCTCCGTTGATCCCGGCC 90

Qy   61 CCTGCTCTCCAGGCCTTCACTGTGTGCAAACTGCTCGTCTGTCTTCTGATGCCTGTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91 CCTGCTCTCCAGGCCTTCACTGTGTGCAAACTGCTCGTCTGTCTTCTGATGCCTGTCCAT 150

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA 180

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Qy   241 CCACCCCGGAGGAGGAGGATCTACCTG 300

(... sequence alignment continues, Query Match 100.0%, 1522 matches ...)

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Qy    211 GATGACCCCACTGGGCGAGAGGAGGATCTGCCCAGTGAAGAGGAGGATCACCCAGAGGAGGAT 270
Db   1321 AGGCAGCACAGGAGGAAGCGGGAACCAAAGGGGGGTGTTGAGCTACCGGCCCCAGCGAGAGGTAGCCCGAG 1380
Db   1351 AGGGCACAGAGAGGGGGAACCAAAGGGGGTGTTGAGCTACCGGCCGCCCAGCGCAGAGGTAGCCCGAG 1410
Qy    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
Db   1381 ACTGGAGCCTTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCCATCTGAGGG 1440
Qy    271 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 330
Db   1411 ACTGGAGCCTTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCCATCTGAGGG 1470
Qy    301 GAAGTTAAGCCTTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCT 360
Db   1441 GGAGCCCGGTTAACTGTCCTGTCCCTGCTCATTATGCCACTTCCTTTTTTAAACTGCCACAGAAAATT 1500
Qy    331 GAAGTTAAGCCTTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCT 390
Db   1471 GGAGCCCGGTTAACTGTCCCTGTCCCTGCTCATTATGCCACTTCCTTTTTAAACTGCCAACAAAATT 1530
Qy    361 GAGGCTCCTGAGAGGCTTCAAGAAGAGACCCCAGAATAAATGCCCACAGGGACAAAGAGGGGAT 420
Db   1531 TTTTAAAAATAAATATTTTATTTAAT 1552
Qy    391 GAGGCTCCTGCAGGAGATCTTCAAGAAGAGACCCCAGAATAAATGCCCACAGGGACAAAGAGGGGAT 450
Qy    421 GACCAGAGTCATTGGCGCTATAGGAGGCGAACCCGCCCTGGGGTGTCCCCAGCCTGC 480
Db   1501 TTTTAAAAATAAATATTTTATTTAAT 1522
Qy    451 GACCAGAGTCATTGGCGCTATAGGAGGCGAACCCGCCCTGGGGTGTCCCCAGCCTGC 510
Db   1531 TTTTAAAAATAAATATTTTATTTAAT 1552
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RESULT 12

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LOCUS       AX332607              1552 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3116 from Patent WO0194629.
ACCESSION   AX332607
VERSION     AX332607.1  GI:18123241
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3116 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match   100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    541 CTGCGCCCCCCTTCCAGTCTCCCGGGTTGGATTATCCGGCCCTCCCGCCGCCTTCTCCGCCGCC 600
Db     31 ACAGTCAGCCGCGCCATGGGCTCCCCTGTGCCCCAGCCCCCTGGCTCCTTCCTGTTTGATCCCGGCC 90

Qy    571 GGGGCGGGGCCCCTTCCAGTCTCCCGGGTGGATTATCCGGCCCTCCCGCCGCCCCCCAGCCTGC 630
Db     61 CCTGCTCCAGGGCCTCACTCTGCAACTGCTGCTGCTTCCACTCTTCGATAGCTCAGCCAT 120

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGGTCCC 660
Db     91 CCTGCTCCAGGGCCTCACTCTGCAACTGCTGCTTCCACTCTTCGATAGCTCAGCCAT 150

Qy    631 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGGTCCC 690
Db    121 CCCCAGAGGTTGCCCCGGAATGCAGGAGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Qy    661 GGGGCGGGAGTACCGGGCTCTCGCATCTGCCTCCTCCCTGCCTTCCAGTCGCAGGTCGTCCCGGC 720
Db    151 CCCCAGAGGTTGCCCCGGAATGCAGGAGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 210

Qy    691 GGGGCGGGAGTACCGGGCTCTCGCATCTGCCTCCTCCCTGCCTTCCAGTCGCAGGTCGTCCCGGC 750
Db    181 GATGACCCACTGGGCGAGAGGATCTGCCCAGTGAAGAGGAGGATCACCCAGAGGAGGAT 240

Qy    721 TCGGAGCACACTGTGGAAGGCCACACTGTTTCCCTGCCGAGATCCAAGTGGTTCACCTCAGC 780
Db    211 GATGACCCACTGGGCGAGAGGATCTGCCCAGTGAAGAGGAGGATCACCCAGAGGAGGAT 270

Qy    751 TCGGAGCACACTGTGGAAGGCCACACTGTTTCCCTGCCGAGATCCAAGTGGTTCACCTCAGC 810
Db    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300

Qy    781 ACCGGCCTTTGCCAGAGTTGACAGAGGCCACGTTTCCCTGCCCGGTTGCTCGTCGCTTG 840
Db    271 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 330

Qy    811 ACCGGCCTTTGCCAGAGTTGACCAGGCCCTTGGGCCGCGCCGGGGGAGGCCTGGCCGTGTTGGCC 870
Db    301 GAAGTTAAGCCTTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACTGTT 360

Qy    841 GCCTTTCTGGGAGGAGGGGGAGGAGAAAACAGTGCCTATGAGAGCAGTTGCTGTCGCTTG 900
Db    331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACTGTT 390

Qy    871 GCCTTTCTGGGAGGAGGGGGCCGGAAGAAAACAGTGCCCTATGAGCAGTTGCTGTCTCGCTTG 930
Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAGGGGGAT 420
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RESULT 13

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LOCUS       AX333244               1552 bp    DNA        linear   PAT 09-JAN-2002
DEFINITION  Sequence 3753 from Patent WO0194629.
ACCESSION   AX333244
VERSION     AX333244.1  GI:18123878
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3753 13-DEC-2001;
            Avalon Pharmaceuticals (US)
            1. .1552
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match   100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity   100.0%;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

[Sequence alignment block between Query (Qy) and Database (Db) sequences, positions 1–1552, with full 100% identity match lines throughout.]

RESULT 14

LOCUS   AX336174   1552 bp   DNA   linear   PAT 09-JAN-2002
DEFINITION Sequence 6683 from Patent WO0194629.
ACCESSION   AX336174
VERSION   AX336174.1 GI:18126893
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE   Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 6683 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES   Location/Qualifiers
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ORIGIN

Query Match   100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACAGTCAGCCGCATGGCTCCCCGTGCCCCCTGGTGCCCCGTGCCTGGCTTCCTTCGTTGGATCCCGGCC 60
Db   31 ACAGTCAGCCGCATGGCTCCCCGTGCCCCCTGGTGCCCCGTGCCTGGCTTCCTTCGTTGGATCCCGGCC 90

Qy   61 CCTGCTCCAGGCCCTCACTGTGCAACTGCGTCGTCGTGCTTCCTTCGTTGATGCCTGTCCAT 120
Db   91 CCTGCTCCAGGCCCTCACTGTGCAACTGCGTCGTCGTGCTTCCTTCGTTGATGCCTGTCCAT 150

Qy 121 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGGGAA 180
Db 151 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGGGAA 210

Qy 181 GATGACCCACTGGGCGGAGGGATCTGCCCAGTGAAGAGATTCACCCAGAGAGGAGGAT 240
Db 211 GATGACCCACTGGGCGGAGGGATCTGCCCAGTGAAGAGATTCACCCAGAGAGGAGGAT 270

Qy 241 CCACCCCGGAGAGGAGGAGGATCTACCTGAGAGGAGGAGGACTACCT 300
Db 271 CCACCCCGGAGAGGAGGAGGATCTACCTGAGAGGAGGAGGACTACCT 330

Qy 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy 361 GAGGCTCCTGGAGATCCCAAGAACCCCAGAGAATAATGCCCACCACAGAACAAAGAAGGGGAT 420
Db 391 GAGGCTCCTGGAGATCCCAAGAACCCCAGAGAATAATGCCCACCACAGAACAAAGAAGGGGAT 450

Qy 421 GACCAGAGAGTCATTGCGGCGTTATGGAGGGGGACCCCAGGGGTGTCCCCAGCCCTGC 480
Db 451 GACCAGAGAGTCATTGCGGCGTTATGGAGGGGGACCCCAGGGGTGTCCCCAGCCCTGC 510

Qy 481 GCGGGCGCCGCGTTCCCCGGTGGATATCCGCGCGCCCCAGCTCGCGCCGCCCCGGCC 540
Db 511 GCGGGCGCCGCGTTCCCCGGTGGATATCCGCGCGCCCCAGCTCGCGCCGCCCCGGCC 570

Qy 541 CTGCGCCCCCTGGAACTCCTGGGGTTCCAGCTCCCGCGCCGCCCTTCGCCCGGCC 600
Db 571 CTGCGCCCCCTGGAACTCCTGGGGTTCCAGCTCCCGCGCCGCCCTTCGCCCGGCC 630

Qy 601 AACAATGGGCCACAGTGTGCAACTGACCCTGCCTTCCTGGGCTAGAGATGGCTTCTGGGTCC 660
Db 631 AACAATGGGCCACAGTGTGCAACTGACCCTGCCTTCCTGGGCTAGAGATGGCTTCTGGGTCC 690

Qy 661 GGGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGACTGGGGGGGCTGAGGTCGGTCGC 720
Db 691 GGGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGACTGGGGGGGCTGAGGTCGGTCGC 750

Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 810

Qy 571 CTGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTCACTGGGGGGGCTAGAGATGGCTTGGGGTCC 630
Db 601 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTTCCTGGGCTAGAGATGGCTTGGGGTCC 660
Db 631 AACAATGGCCACAGTGTGCAACTGACCCTGCCTTCCTGGGCTAGAGATGGCTTGGGGTCC 690

Qy 661 GGGGCGGGAGTACCGGGGCTCTCGCAGCTGCATCTCACTGGGGGGGGCTGCAGGTCGTCGTCCTCCGGGC 720
Db 691 GGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTGACTGGGGGGGCTGCAGGTCGTCGTCCTCCGGGC 750

Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 810

Qy 781 ACCGCCCTTTGCCAGAGTTGACGAGGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 840
Db 811 ACCGCCCTTTGCCAGAGTTGACGAGGGCCCTTGGGGGCCCGGGGGGCCCCGGGGCCCC 870

Qy 841 GCCTTTTCTGGGAGGAGGGGCCCGGAAGAAAACAGTGGCCTAATGAGAGTTGCTTGCTTGCTTG 900
Db 871 GCCTTTTCTGGGAGGAGGGGCCCGGAAGAAAACAGTGGCCTAATGAGAGTTGCTTGCTTGCTTG 930

Qy 901 GAAGAAAATCGCTGAGGAAGGCTCAGGACTCAGGTCCCAGGACTGAGCAGTTGGACTGTGTCTGTCTGCGGTTG 960
Db 931 GAAGAAAATCGCTGAGGAAGGCTCAGGACTCAGGTCCCAGGACTGAGCAGTTGGACTGTGTCTGTCTGCGGTTG 990

Qy 961 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGATCAGTGGGGTCTTCTGACTACACCGCCCCTGT 1020
Db 991 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGATCAGTGGGGTCTTCTGACTACACCGCCCCTGT 1050

Qy 1021 GCCCAGGGGTGTCATTCTGACTGTGTTTAACCAGACAGTGATGTGAGTGGGGTCTTCTGACTACACCGCCCTC 1080
Db 1051 GCCCAGGGGTGTCATTCTGACTGTGTTTAACCAGACAGTGATGTGAGTGGGGTCTTCTGACTACACCGCCCTC 1110

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REFERENCE   1  (bases 1 to 1552)
  AUTHORS   Pastorek,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUN-1992) J. Pastorek, Institute of Virology, Slovak
            Academy of Sciences, Dubravska 9, 842 46 Bratislavia, SLOVAK
            REPUBLIC
  REMARK    revised by [3] MAT
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REFERENCE   2  (bases 1 to 1552)
  AUTHORS   Pastorek,J., Pastorekova,S., Callebaut,I., Mornon,J., Zelnik,V.,
            Opavsky,R., Zatovicova,M., Liao,S., Portetelle,D., Stanbridge,E.J.,
            Zavada,J. and Burny,A.
  TITLE     Cloning and characterization of MN, a human tumor-associated
            protein with a domain homologous to carbonic anhydrase and a
            putative helix-loop-helix DNA binding segment
  JOURNAL   Oncogene 9 (10), 2877-2888 (1994)
  MEDLINE   94366734
  PUBMED    8084592
REFERENCE   3  (bases 1 to 1552)
  AUTHORS   Pastorek,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-1994) J. Pastorek, Institute of Virology, Slovak
            Academy of Sciences, Dubravska 9, 842 46 Bratislavia, SLOVAK
            REPUBLIC
  REMARK    revised by [4] MAT
REFERENCE   4  (bases 1 to 1552)
  AUTHORS   Pastorek,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-1995) J. Pastorek, Institute of Virology, Slovak
            Academy of Sciences, Dubravska 9, 842 46 Bratislavia, SLOVAK
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ORIGIN
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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9	1522	100.0	1522	6	ABL68346	Abl68346 Kidney ca
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FT                                     Location/Qualifiers
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KW   MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;
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DT   19-AUG-1996  (first entry)
DT   25-MAR-2003  (revised)
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PA   (CIBA ) CIBA CORNING DIAGNOSTICS CORP.
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PR   07-JUN-1995; 95US-00487077.
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PR   07-JUN-1995; 95US-00485049.
PR   07-JUN-1995; 95US-00481658.
PR   15-JUN-1995; 95US-00481504.
PR   15-JUN-1994; 94US-00260190.
PP   15-JUN-1995; 95WO-US007628.
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XX
PT   MN gene, protein and nucleic acid fragments - used as primers and probes
PT   in the detection of MN antigens and antibodies, and in the treatment of
PT   (pre)neoplastic disease.
XX
PS   Claim 1; Fig 1; 102pp; English.
XX
CC   The present sequence is the full length MuTu endogenous cellular
CC   component, MN, cDNA clone, which was isolated from lymphocytic
CC   choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV, the
CC   exogenous MuTu transmissible agent (MX), Infection increases the
CC   expression level of the MN gene. MN is a putative oncogene, and can
CC   therefore be used in the development of prods. for the diagnosis and
CC   treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC   treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC   antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC   vaccine contg. immunogenic amounts of the MN protein can be used to
CC   immunise a vertebrate against a NP disease associated with MN antigen
CC   expression. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match          100.0%;  Score 1522;  DB 2;  Length 1522;
Best Local Similarity  100.0%;  Pred. No. 0;  Mismatches 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ACAGTCAGCGCACATGGCTCCCTCCCCGTTCCCTCTTGTTGATCCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCGCACATGGCTCCCTCCCCGTTCCCTCTTGTTGATCCCCGGCC 60

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT 120

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCGTTGGGAGAGGGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCGTTGGGAGAGGGGAA 180

Qy    181 GATGACCCACTGGGCGACGGAGGATCTGCCCAGTCAAGAGAGGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGACCCACTGGGCGACGGAGGATCTGCCCAGTCAAGAGAGGAGGAGGAT 240

Qy    241 CCACCCCGAGAGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGACCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACCCCGAGAGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGACCT 300

Qy    301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGTAGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGTAGGA 360

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAA 420

Qy    421 GACCAGAGTCATTGGGCGCTTATGGAGGGCACCCGGCCCTGGCCCCCAGCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GACCAGAGTCATTGGGCGCTTATGGAGGGCACCCGGCCCTGGCCCCCAGCT 480

Qy    481 GCGGGGCCGGCTTCCAGTGGGGAATATCCGGCCCTTCTGCCCCGGCC 540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCGGGGCCGGCTTCCAGTGGGGAATATCCGGCCCTTCTGCCCCGGCC 540

Qy    541 CTGCGCCCCTGGAACTCCTGGGCTTCAGCTCCCGGCTCCGGACTGCCCTGCGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGCGCCCCTGGAACTCCTGGGCTTCAGCTCCCGGCTCCGGACTGCCCTGCGC 600

Qy    601 AACAATGCCCACAGTGTGCAACTGACCCTGGGCTTCGGGGTCTCCGGGC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACAATGCCCACAGTGTGCAACTGACCCTGGGCTTCGGGGTCTCCGGGC 660

Qy    661 GGGCGGGGAGTACCGGGCGCTCGAGCTGCAGGTCGTCCGGGC 720
          ||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGCGGGGAGTACCGGGCGCTCGAGCTGCAGGTCGTCCGGGC 720
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Qy    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCTCGTGGTTCACTCAGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCTCGTGGTTCACTCAGC 780

Qy    781 ACCGGCCTTTGCCAGAGTGACGAGGCCTTGGGCGCGCCCGGGAGGCC 840
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACCGGCCTTTGCCAGAGTGACGAGGCCTTGGGCGCGCCCGGGAGGCC 840

Qy    841 GCCTTTCTTCGGAGGAGGGCCCGGAGAGAAACAGTGCCTATGAGCAGTTGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GCCTTTCTTCGGAGGAGGGCCCGGAGAGAAACAGTGCCTATGAGCAGTTGC 900

Qy    901 GAAGAAATCGGCTGAGGAAGGCCTCAGAGACTCAGGTGGGACATATCTGCAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAAGAAATCGGCTGAGGAAGGCCTCAGAGACTCAGGTGGGACATATCTGCAC 960

Qy    961 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCCTGACT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCCTGACT 1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTAACCAGACAGTGAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGGTGTCATCTGGACTGTGTTAACCAGACAGTGAGTGCTAAGCAGCTC 1080

Qy   1081 CACACCCTCTCTGACACCCTGGTGGGACCTGGTCGGTCTACAGCTGAACTTCCGA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCTCTCTGACACCCTGGTGGGACCTGGTCGGTCTACAGCTGAACTTCCGA 1140

Qy   1141 GCGACGCAGCCTTTGAATGGGCGGACCTCCTTCCCCTGCTTCGGGGTGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCTTTGAATGGGCGGACCTCCTTCCCCTGCTTCGGGGTGGACAGC 1200

Qy   1201 AGTCCTCGGGCCTGCTGAGCCAGTCCAGCTGAATTCCTGCCGGCCTGCTGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCCTCGGGCCTGCTGAGCCAGTCCAGCTGAATTCCTGCCGGCCTGCTGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTGGCCCTCCTTTTGCGTCGTCACCGAGCCGGTCGCGGTTCGAGATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCTGGTTTTGGCCCTCCTTTTGCGTCGTCACCGAGCCGGTCGCGGTTCGAGATGAGA 1320

Qy   1321 AGGCAGCACAGAAGGGGACCAAAAGGGGTGTGAGCTACCGCGCAGGAGTTAGCCCGAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGCAGCACAGAAGGGGACCAAAAGGGGTGTGAGCTACCGCGCAGGAGTTAGCCCGAG 1380

Qy   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGCCATCTGAGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGCCATCTGAGGG 1440

Qy   1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTAGGCCACTTCCTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTAGGCCACTTCCTTTAACTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAATATTTATAAT 1522
          ||||||||||||||||||||||
Db   1501 TTTTAAAATAAATATTTATAAT 1522
```

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RESULT 2
AAA16540
ID   AAA16540 standard; cDNA; 1522 BP.
XX
AC   AAA16540;
XX
DT   16-JUN-2000  (first entry)
XX
DE   Human MN protein encoding cDNA SEQ ID NO:1.
XX
KW   Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW   oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW   MN/CA IX isoenzyme; d8.
XX
OS   Homo sapiens.
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XX
PN   US6027887-A.
XX
PD   22-FEB-2000.
XX
PF   24-JAN-1997;   97US-00787739.
XX
PR   21-OCT-1992;   92US-00964589.
PR   30-DEC-1993;   93US-00177093.
PR   15-JUN-1994;   94US-00260190.
PR   07-JUN-1995;   95US-00477504.
PR   07-JUN-1995;   95US-00481658.
PR   07-JUN-1995;   95US-00485049.
PR   07-JUN-1995;   95US-00485862.
PR   07-JUN-1995;   95US-00485863.
PR   07-JUN-1995;   95US-00486756.
PR   07-JUN-1995;   95US-00487077.
XX
PA   (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI   Pastorek J,  Zavada J,  Pastorekova S;
XX
DR   WPI; 2000-194827/17.
DR   P-PSDB; AAY53228.
XX
PT   Nucleic acid based assay for diagnosing a wide variety of
PT   preneoplastic/neoplastic disease comprises screening for the presence of
PT   abnormal MN gene expression in a vertebrate.
XX
PS   Claim 1; Fig 1; 87pp; English.
XX
CC   The present invention describes a method of screening for
CC   preneoplastic/neoplastic disease. The method comprises: (1) determining
CC   whether abnormal MN gene expression is present in a vertebrate; and (2)
CC   if abnormal MN gene expression is determined to be present in the
CC   vertebrate, determining that the vertebrate has a significant risk of
CC   having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC   encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC   protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC   is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC   in a vertebrate, preferably a human. The disease detected is mammary,
CC   bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC   vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC   testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC   duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC   mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC   mucosa, pancreatic duct epithelium or liver duct epithelium
CC   preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC   AAY53245 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1522;  DB 3;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 ACAGTCAGCGCCGCATGGCTCCCCTTGTGCCCCAGCCTCCCGTTCTCGTTGATCCCGGCC    60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ACAGTCAGCGCCGCATGGCTCCCCTTGTGCCCCAGCCTCCCGTTCTCGTTGATCCCGGCC    60

Qy        61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTGCTTCTGATGCCTGTCCAT         120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTGCTTCTGATGCCTGTCCAT         120

Qy       121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGACGAGGAGGAA          180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGACGAGGAGGAA          180

Qy       181 GATGACCCACTGGGCGAGGAGGAGAGAGGAATCTGCCCAGTGAAGAGGAGGAGGAGGAT    240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GATGACCCACTGGGCGAGGAGGAGAGAGGAATCTGCCCAGTGAAGAGGAGGAGGAGGAT    240

Qy       241 CCACCCCGGAGGAGGAGGAGGATCTACCTGGAGAGGAGGAGGAGGATCTACCT       300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCACCCCGGAGGAGGAGGAGGATCTACCTGGAGAGGAGGAGGAGGATCTACCT       300

Qy       301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAAGAGGAGGATCTACTGTT    360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAAGAGGAGGATCTACTGTT    360

Qy       361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGAAGAGGGAT    420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGAAGAGGGAT    420

Qy       421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGTGTCCCCAGCCTGC    480
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGTGTCCCCAGCCTGC    480

Qy       481 GCGGGCCGGGAGTTCCCAGTCTCCCGGGTGGAATATCCGCGCGCCCTTCTGCCCGGGGC    540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCGGGCCGGGAGTTCCCAGTCTCCCGGGTGGAATATCCGCGCGCCCTTCTGCCCGGGGC    540

Qy       541 CTGCCGCCCCCCTTGGGAACTCCTGGCCTTCCCAGCTCCCGCCCGCTCCCAGAACCTGCGC    600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CTGCCGCCCCCCTTGGGAACTCCTGGCCTTCCCAGCTCCCGCCCGCTCCCAGAACCTGCGC    600

Qy       601 AACAAATGGGCACACACTGTGTGCAACTGACCCCTGCCTTCCTGGCTAGAGTGGCTCCTGGGCTCCC    660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AACAAATGGGCACACACTGTGTGCAACTGACCCCTGCCTTCCTGGCTAGAGTGGCTCCTGGGCTCCC    660

Qy       661 GGGCCGGGAGTACCGGGCCTTGCAGGTGCATCTGACACTGGGGGGGCTGCAGGTCGTCCGGGC    720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGGCCGGGAGTACCGGGCCTTGCAGGTGCATCTGACACTGGGGGGGCTGCAGGTCGTCCGGGC    720

Qy       721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGCGTTCACCTGAGC    780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGCGTTCACCTGAGC    780

Qy       781 ACCGGCCTTTGCCCAGAGTTGACGAGCCCTTGGGGCCCGCCCCGGAGGCCTGTGGGCC    840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ACCGGCCTTTGCCCAGAGTTGACGAGCCCTTGGGGCCCGCCCCGGAGGCCTGTGGGCC    840

Qy       841 GCCTTTCTGGAGGAGGGGCCCGGAGAAAAACAGTGCCTATGAGCAGTTGCGTGTCTGCTTG    900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCCTTTCTGGAGGAGGGGCCCGGAGAAAAACAGTGCCTATGAGCAGTTGCGTGTCTGCTTG    900

Qy       901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC    960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC    960

Qy       961 CTGCCCCTCTGACTTCAGCCGCCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCGT   1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 CTGCCCCTCTGACTTCAGCCGCCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCGT   1020

Qy      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAGTGCGTAAGCAGCTC   1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAGTGCGTAAGCAGCTC   1080

Qy      1081 CACACCCTCTCTGACACCCTGTGGGACCTGGTGACTCTCGGCGTTGAACTTCCGA   1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CACACCCTCTCTGACACCCTGTGGGACCTGGTGACTCTCGGCGTTGAACTTCCGA   1140

Qy      1141 GCGACGCAGCCTTTGAAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGGACAGC   1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GCGACGCAGCCTTTGAAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGGACAGC   1200

Qy      1201 AGTCCTCGGGCGCTGCTGAGCCAGTCGAGTTCAGCGAATTCCTGCTGGTTGACATCCTA   1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 AGTCCTCGGGCGCTGCTGAGCCAGTCGAGTTCAGCGAATTCCTGCTGGTTGACATCCTA   1260

Qy      1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTGTCACCAGCGTGCGGATGAGA   1320
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTGTCACCAGCGTGCGGATGAGA   1320

Qy      1321 AGGCAGCACAGAAGGGGACCAAAGGGGGTTGTGAGCTACCGGCGCAGAGGTAGCCGAG   1380
```

RESULT 3

AAA52459

ID   AAA52459 standard; cDNA; 1522 BP.
XX
AC   AAA52459;
XX
DT   25-SEP-2000 (first entry)
XX
DE   Human MN cDNA.
XX
KW   MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW   proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW   abnormal expression; neoplastic disease; cancer; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   13..1392
FT   /*tag= a
FT   /product= "Human MN protein"
XX
PN   WO20024913-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999; 99WO-US024879.
XX
PR   23-OCT-1998; 98US-00177776.
PR   23-OCT-1998; 98US-00178115.
XX
PA   (FARB) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J, Pastorekova S, Pastorek J;
XX
DR   WPI; 2000-350752/30.
DR   P-PSDB; AAB03005.
XX
PT   A molecule which specifically binds to a site on MN protein (oncoprotein)
PT   and prevents adhesion of vertebrate cells to the protein, useful for
PT   treating preneoplastic or neoplastic diseases such as cancer.
XX
PS   Example 1; Fig 1A-C; 154pp; English.
XX
CC   The invention relates to the inhibition of cell adhesion mediated by the
CC   MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC   protein). The MN protein is a tumour-associated adhesion molecule which
CC   comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC   protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC   Abnormal expression of the MN protein is associated with tumorigenicity.
CC   The invention encompasses MN protein molecules (e.g. proteins and peptides)
CC   which specifically bind to a site on the MN protein, thereby preventing
CC   adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC   also encompasses MN proteins or MN protein fragments which can be added
CC   to the extracellular environment to prevent the adhesion of vertebrate
CC   cells to each other. The invention also relates to the identification of
CC   the binding site of the MN protein and to a method of identifying a site
CC   on an MN protein to which cells adhere, comprising testing a series of
CC   overlapping peptides from the protein in a cell adhesion assay. The
CC   invention encompasses a vector comprising an expression control sequence
CC   operatively linked to a nucleic acid encoding the variable domain of a
CC   MN-specific antibody, where the domains are separated by a flexible
CC   linker peptide (AAB03035) and the vector inhibits the growth of a
CC   vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC   protein. The invention also encompasses a vector comprising a nucleic
CC   acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC   gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC   neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC   gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC   and peptides, and expression vectors encoding such proteins and peptides
CC   are useful for treating patients with preneoplastic or neoplastic disease
CC   (e.g. cancers) associated with or characterised by abnormal MN
CC   expression. The present sequence represents cDNA encoding the human MN
CC   protein
XX
SQ   Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match   100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ACAGTCAGCGCGATCAGGCTCTCCCCTGCCCCAGCCCCTGCCCCTGTGGGGATCCCCGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACAGTCAGCGCGATCAGGCTCTCCCCTGCCCCAGCCCCTGCCCCTGTGGGGATCCCCGCC 60

Qy         61 CCTGCTCCAGGCCCTCACTGTGCAAACTGCTGTGCTGTCACTGTCGTGTCCATGTGTCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGCTCCAGGCCCTCACTGTGCAAACTGCTGTGCTGTCACTGTCGTGTCCATGTGTCCAT 120

Qy        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTCTTGGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTCTTGGGAA 180

Qy        181 GATGACCCCACTGGGCGCGAGGAGGAGGATCTGCCCAGTGAAGAGGAGTCACCCAGAGGAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGACCCCACTGGGCGCGAGGAGGAGGATCTGCCCAGTGAAGAGGAGTCACCCAGAGGAGGAT 240

Qy        241 CCACCCGGAGAGGAGGATCTACCTGGAGGATTACCTGGAGAGGAGGAGGAGGATCTACCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACCCGGAGAGGAGGATCTACCTGGAGGATTACCTGGAGAGGAGGAGGAGGATCTACCT 300

Qy        301 GAAGTTAAGCCTAAATCAGAAGAGGAGGGCTCCCTGAAGTTAGAGGAGGACTACCTACTGTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAAGTTAAGCCTAAATCAGAAGAGGAGGGCTCCCTGAAGTTAGAGGAGGACTACCTACTGTT 360

Qy        361 GAGGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACCAGGGACACAAAGAAGGAGGAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACCAGGGACACAAAGAAGGAGGAT 420

Qy        421 GACCAGAGTCATTGGGCGGCTATGGGAGGGGACCCGCCCCTGGCCCCCGGGGTGTCCCCAGCCTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GACCAGAGTCATTGGGCGGCTATGGGAGGGGACCCGCCCCTGGCCCCCGGGGTGTCCCCAGCCTGC 480

Qy        481 GCGGGCCCGCTTCCAGTCCCCGGTGGATATCCGCGCCTGCCCCGGGCCTTCGCCCCAGCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCGGGCCCGCTTCCAGTCCCCGGTGGATATCCGCGCCTGCCCCGGGCCTTCGCCCCAGCCC 540

Qy        541 CTGCGCCCCCTGGAACTCCTCGGCTTCCAGCTCCCAGTCCCCAGAACTGCGCCTGCGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCGCCCCCTGGAACTCCTCGGCTTCCAGCTCCCAGTCCCCAGAACTGCGCCTGCGC 600

Qy        601 AACAATGGCCACAGTGTGCAACTGACACCTGCCTTCCTGGGCTAGAGATGGCTGGGGTCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACAATGGCCACAGTGTGCAACTGACACCTGCCTTCCTGGGCTAGAGATGGCTGGGGTCC 660

Qy        661 GGGCGGGAGTACCGGCTCTGCAACTGACCCTGCCTCCTGGGCTAGGGGGCTTCGTCCGGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGCGGGAGTACCGGGCTCTGCAGCTCCATCTGCACTGGGGGCTGCGAGGTCGGTCCGGGC 720

Qy        721 TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCGAGGATCCACGTGGGTTCACCTCAGC 780
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Db    721  TCCGGAGCACTGTGGGAAGGCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    780  ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCGCCTGCCGTGCCGTTGGCC
Db    781  ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCGCCTGCCGTGCCGTTGGCC    840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841  GCCTTTCTGGAGCGGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCGCTTG
Db    841  GCCTTTCTGGAGCGGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCGCTTG    900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901  GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACATATCTGCACTC
Db    901  GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACATATCTGCACTC    960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961  CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTTCTCTTGACTTACACGCCCCTGT
Db    961  CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTTCTCTTGACTTACACGCCCCTGT   1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021  GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTTAAGCAGCTC
Db   1021  GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTTAAGCAGCTC   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081  CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA
Db   1081  CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA   1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141  GCCACGCGACACCTTTGAAATGGGCGAGTGATTGAGCTCCTTCCTTCCTTGCTGGGAGTGGACAGC
Db   1141  GCCACGCGACACCTTTGAAATGGGCGAGTGATTGAGCTCCTTCCTTCCTTGCTGGGAGTGGACAGC   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201  AGTCCTCGGGCTGCTGAGCGTCAGCAGTTCCTGCCTGGGTTTGTGCAGCATCCTA
Db   1201  AGTCCTCGGGCTGCTGAGCGTCAGCAGTTCCTGCCTGGGTTTGTGCAGCATCCTA   1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261  GCCCTGGTTTTTGGCCTCCTTTTTGCTGCGTTCCTTGTCAGGATGAGA
Db   1261  GCCCTGGTTTTTGGCCTCCTTTTTGCTGCGTTCCTTGTCAGGATGAGA   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321  AGGCAGCAGCACAGAGAGAGGGGAACCAAAGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG
Db   1321  AGGCAGCAGCACAGAGAGAGGGGAACCAAAGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG   1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381  ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGGAAGCCAGCCAGGCATCTGAGGG
Db   1381  ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGGAAGCCAGCCAGGCATCTGAGGG   1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441  GGAGCCGGTAACTGTCCTCCTCTCATTATGCCACTTCCTTTTAACTGCAAGAAAATT
Db   1441  GGAGCCGGTAACTGTCCTCCTCTCATTATGCCACTTCCTTTTAACTGCAAGAAAATT   1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501  TTTTAAAATAAATATATTTATAAT
Db   1501  TTTTAAAATAAATATTTATAAT   1522
```

```
Qy     1  ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCCTGTGTTGATCCCGGCC     60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCCTGTGTTGATCCCGGCC     60
Qy    61  CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTCTGTCACTGCCCTTCGATGGTCCCCAT    120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTCTGTCACTGCCCTTCGATGGTCCCCAT    120
Qy   121  CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGCTCTTCTGGGGAA    180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCTTGCTCCAGGCCTCACTGTGCAACTGCTGCTCTTCTGATCCCTGCTCTTCCAT    120
Qy   181  GATGACCCACTGGGCCGCAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGGAGGAT    240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GATGACCCACTGGGCCGCAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGGAGGAT    240
Qy   241  CCACCCGGAGGAGGAGGGGGATCTACCTGGAGGAGGAGGAGGAGGAGGATCTACCT    300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CCACCCGGAGGAGGAGGGGGATCTACCTGGAGGAGGAGGAGGAGGAGGATCTACCT    300
Qy   301  GAAGTTAAGCCTAAATCAGGAAGAGAGTGGGCTTCCCTGAAGTTAGAGGATCTACCTG    360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GAAGTTAAGCCTAAATCAGAGAAGAGAGAGGGGAATCTCCCTGAAGTTAGAGAGGATCTACCTGTT    360
Qy   361  GAGGCTCCTGAGATCCTCAAGAACACCCAGAATAATGCCCACAGGGACAAAGAAGAGGGAT    420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GAGGCTCCTGAGATCCTCAAGAACACCCAGAATAATGCCCACAGGGACAAAGAAGAGGGAT    420
```

```
Db   361 GAGGCTCCTCTGGAGGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420

Qy   421 GACCAGAGTCATTGGCGCTATGAGGGGACCCGGCCCCCGGGTGTCCCCAGCCTGC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGAGTCATTGGCGCTATGAGGGGACCCGGCCCCCGGGTGTCCCCAGCCTGC 480

Qy   481 GCGGGGCCCCTTCCAGTCTCCCGGTGGATATCCGGCCCCCCGGCCTCGCCCCGCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCGGGGCCCCGTTCCAGTCCCCGGTGGATATCCGGCCCCCCGGCCTCGCCCCGCC 540

Qy   541 CTGCGCCCCCCTGGAACTCCTGGGGCTTCAGCTGCTGCCCCAGAACCTGGCCGCC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGCGCCCCCTGGAACTCCTGGGGCTTCAGCTGCTGCCCCAGAACCTGGCCGCC 600

Qy   601 AACAATGGCCACAGTGTGCAACTGAACCCTGCCTTCCTGGGCCTAGAGATGGCTC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACAATGGCCACAGTGTGCAACTGAACCCTGCCTTCCTGGGCCTAGAGATGGCTC 660

Qy   661 GGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGC 720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGGAGATCCACGTGGTTCA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGGAGATCCACGTGGTTCA 780

Qy   781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCGCCCGGGGAGGCCCTGGCC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCGCCCGGGGAGGCCCTGGCC 840

Qy   841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTTATGAGCAGTTGCTGCTC 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTTATGAGCAGTTGCTGCTC 900

Qy   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTG 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTG 960

Qy   961 CTGCCCTTCTGACTTCAGCCGCTACTTCCAAATATGAGAGGGGTCTCTGACTACA 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CTGCCCTTCTGACTTCAGCCGCTACTTCCAAATATGAGAGGGGTCTCTGACTACA 1020

Qy  1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGGTGCTG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGGTGCTG 1080

Qy  1081 CACACCCTCTCTGACACCCTGTGTGGGACCTGGTGACTCTCGGGTACAGCTGAAC 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CACACCCTCTCTGACACCCTGTGTGGGACCTGGTGACTCTCGGGTACAGCTGAAC 1140

Qy  1141 GCGGACGGCAGCCTTTGAATGGGCGAGTGATTGAGGGCTTCCCTTCCCTGCTCCG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCGGACGGCAGCCTTTGAATGGGCGAGTGATTGAGGGCTTCCCTTCCCTGCTCCG 1200

Qy  1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTCGGCCTGGCTGCTGACATCCTA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTCGGCCTGGCTGCTGACATCCTA 1260

Qy  1261 GCCCTGGTTTTTTGGGCTTCCCTTTTGCGTGTCACCAGCGTTCCTTGTGTCAGATGAGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GCCCTGGTTTTTTGGGCTTCCCTTTTGCGTGTCACCAGCGTTCCTTGTGTCAGATGAGA 1320

Qy  1321 AGGCAGCACAGAGAGGGAACCAAAGGGAGGGTGTGAGCTTACCGGCCGCAGAGGTAGCCGAG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGGCAGCACAGAGAGGGAACCAAAGGGAGGGTGTGAGCTTACCGGCCGCAGAGGTAGCCGAG 1380

Qy  1381 ACTGGAGCCTAGAGGCTTGGAATCTTGGAGAATGTGAGGAGCCATCCAGAGGGCATTCTGAGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 ACTGGAGCCTAGAGGCTTGGAATCTTGGAGAATGTGAGGAGCCATCCAGAGGGCATTCTGAGGG 1440

Qy  1441 GGAGCCCGGTAACTGTCTGTTCCTGCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GGAGCCCGGTAACTGTCTGTTCCTGCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Qy  1501 TTTTAAAATAAAATATTTATAAT 1522
         |||||||||||||||||||||||
Db  1501 TTTTAAAATAAAATATTTATAAT 1522
```

Db Human MN gene sequence SeqID1.

RESULT 5
ADK41803
ID   ADK41803 standard; DNA; 1522 BP.
XX
AC   ADK41803;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Human MN gene sequence SeqID1.
XX
KW   carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
KW   human; vertebrate; cytostatic; vaccine; gene therapy;
KW   renal cell carcinoma; breast cancer; colorectal cancer; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   13..1392
FT   /*tag= a
FT   /product= "Human MN protein"
XX
PN   WO2004005348-A1.
XX
PD   15-JAN-2004.
XX
PF   22-FEB-2003; 2003WO-US005137.
XX
PR   23-MAY-2002; 2002US-0383068P.
PR   05-DEC-2002; 2002US-0431499P.
XX
PA   (FARB) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J, Pastorekova S, Pastorek J, Zavadova Z;
XX
DR   WPI; 2004-083500/08.
DR   P-PSDB; ADK41804.
XX
PT   New soluble form of the carbonic anhydrase IX (CA IX) protein for
PT   screening, diagnosing or prognosing diseases associated with abnormal
PT   expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
PT   colorectal cancer.
XX
PS   Disclosure; SEQ ID NO 1; 159pp; English.
XX
CC   This invention relates to a novel soluble form of the carbonic anhydrase
CC   IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
CC   precancerous and/or cancerous cells of a vertebrate into a body fluid.
CC   The invention may be useful for the development of compounds with a
CC   cytostatic activity or a vaccine whilst the disclosed sequences may be
CC   used for gene therapy. The protein and method are useful for screening,
CC   diagnosing or prognosing diseases associated with abnormal expression of
CC   carbonic anhydrase IX protein, such as precancerous and cancerous
CC   diseases like renal cell carcinoma, breast cancer or colorectal cancer.
CC   The monoclonal antibody may also be used for treating or preventing
CC   precancerous and cancerous diseases. The present sequence is that of the
CC   gene which encodes the human MN protein of the invention.
XX
SQ   Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

```
Qy     1 ACAGTCAGCCGCCGCATGGCTCCCCTGTGGCCCCAGCCCCTCGTTGATCCCGGCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ACAGTCAGCCGCCGCATGGCTCCCCTGTGGCCCCAGCCCCTCGTTGATCCCGGCC 60
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Query Match   100.0%; Score 1522; DB 12; Length 1522;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   61 CCTGCTCTTCCAGGGCCTCACTGTGTGCAACTGCTCTGCTCTCACTGCTTCATGAATGCCTGTGTCCAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTGCTCTTCCAGGGCCTCACTGTGTGCAACTGCTCTGCTCTCACTGCTTCATGAATGCCTGTGTCCAT 120

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGGATTCCCCCCTTGGGAGGAGGGCTCTTCTGGGGAA 180
Db   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGGATTCCCCCCTTGGGAGGAGGGCTCTTCTGGGGA 180

Qy   181 GATGACCCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGAGGAGGAT 240
Db   181 GATGACCCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGAGGAGGAT 240

Qy   241 CCACCCCGAGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
Db   241 CCACCCCGAGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300

Qy   301 GAAGTTAAGCCTAAATCAGAGAGAAGAGGAGGCTCCCTGAAGTTAGGAGGATCTACCTACTGTT 360
Db   301 GAAGTTAAGCCTAAATCAGAGAGAAGAGGAGGCTCCCTGAAGTTAGGAGGATCTACCTACTGTT 360

Qy   361 GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGGACAAAGAAAGGGGAT 420
Db   361 GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGGACAAAGAAAGGGGAT 420

Qy   421 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCCCTCGGCCCTGGCCCGGGTGTCCCAGCCCTGC 480
Db   421 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCCCTCGGCCCTGGCCCGGGTGTCCCAGCCCTGC 480

Qy   481 GCGGGCGCCCTTCCAGTCCCCGGTGGATATCCGGCCCCCCAGCTCTGCCGCCCTTTCTGCCCCGGCC 540
Db   481 GCGGGCGCCCTTCCAGTCCCCGGTGGATATCCGGCCCCCCAGCTCTGCCGCCCTTTCTGCCCCGGCC 540

Qy   541 CTGCGCGCCCCTGGAACTCCTGGGCGTTCAGCCTCCCAGCTCCCCGGAACTGCGCGCTGGGCCC 600
Db   541 CTGCGCGCCCCTGGAACTCCTGGGCGTTCAGCCTCCCAGCTCCCCGGAACTGCGCGCTGGGCCC 600

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGCTCCTGGGGCTAGAGATGGCTCTGGGGTCCC 660
Db   601 AACAATGGCCACAGTGTGCAACTGACCCTGCTCCTGGGGCTAGAGATGGCTCTGGGGTCCC 660

Qy   661 GGGCCGGGAGTACCGGGGCTTCTGCAGCTGCATCTGGGGGGGCTGCAGGTCGTCGTCCGGGC 720
Db   661 GGGCCGGGAGTACCGGGGCTTCTGCAGCTGCATCTGGGGGGGCTGCAGGTCGTCGTCCGGGC 720

Qy   721 TCGGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCGAGATCCACGTGTGTTCACCTCAGC 780
Db   721 TCGGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCGAGATCCACGTGTGTTCACCTCAGC 780

Qy   781 ACGGCCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCGCCCGGGGCCTGGCCGTGGTTGGCC 840
Db   781 ACGGCCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCGCCCGGGGCCTGGCCGTGGTTGGCC 840

Qy   841 GCCTTTCTTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
Db   841 GCCTTTCTTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900

Qy   901 GAAGAAAATCGGCTGAGGAGAGGCTCAGGACTTCAGGTCCCAGGGACTGGGACATAATCTGCACTC 960
Db   901 GAAGAAAATCGGCTGAGGAGAGGCTCAGGACTTCAGGTCCCAGGGACTGGGACATAATCTGCACTC 960

Qy   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTACACGGCCCCTGT 1020
Db   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAATATGAGGGGTCTCTGACTACACGGCCCCTGT 1020

Qy 1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTAGCAGCTC 1080
Db 1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTAGCAGCTC 1080

Qy 1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTCGTACTCTCGGGCTACAGCTGAACTTCCGA 1140
Db 1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTCGTACTCTCGGGCTACAGCTGAACTTCCGA 1140

Qy 1141 GCGACGGCCAGCCTTTGAAATGGGCGGACAGTGATTGAGCGCCTCCTTCCTTCCCTTGCTGGGAGTGGGACAGC 1200
Db 1141 GCGACGGCCAGCCTTTGAAATGGGCGGACAGTGATTGAGCGCCTCCTTCCTTCCCTTGCTGGGAGTGGGACAGC 1200

Qy 1201 AGTCCTTCCGGGCGCTGCTGAGCCCAGAGTCCAGCTGAAATTCCTGCCTGTGCTGCTGCTGACAATCCTA 1260
Db 1201 AGTCCTTCCGGGCGCTGCTGAGCCCAGAGTCCAGCTGAAATTCCTGCCTGTGCTGCTGCTGACAATCCTA 1260

Qy 1261 GCCCTGGGTTTTGGGCCTCCTTTTTGCTGTGACCACCGTCGCGGTTCCTTGTGCAGATGAGA 1320
Db 1261 GCCCTGGGTTTTGGGCCTCCTTTTTGCTGTGACCACCGTCGCGGTTCCTTGTGCAGATGAGA 1320

Qy 1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTTGAGCTACCGGCGCAGCAGAGGTAGCCGAG 1380
Db 1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGTGTTGAGCTACCGGCGCAGCAGAGGTAGCCGAG 1380

Qy 1381 ACTGGAGCCTAGAGGCTGGAATCTTGGAGAATGTGAGAGGCCAGCAGCATCTGAGGG 1440
Db 1381 ACTGGAGCCTAGAGGCTGGAATCTTGGAGAATGTGAGAGGCCAGCAGCATCTGAGGG 1440

Qy 1441 GGAGCGCGGTAAACTGTCCTGTCCTGGCTCATTAATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
Db 1441 GGAGCGCGGTAAACTGTCCTGTCCTGGCTCATTAATGCCACTTCCTTTTAACTGCCAAGAAATT 1500

Qy 1501 TTTTAAAATAAAATATTTTATAAT 1522
Db 1501 TTTTAAAATAAAATATTTTATAAT 1522

RESULT 6

ABL64779
ID   ABL64779 standard; DNA; 1552 BP.
XX
AC   ABL64779;
XX
DT   15-MAY-2002 (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:3116.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20019462-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
PR   05-JUN-2000; 200US-0209473P.
PR   05-JUN-2000; 200US-0209531P.
PR   18-SEP-2000; 200US-0233133P.
PR   18-SEP-2000; 200US-0233617P.
PR   20-SEP-2000; 200US-0234009P.
PR   20-SEP-2000; 200US-0234034P.
PR   20-SEP-2000; 200US-0234052P.
PR   22-SEP-2000; 200US-0245509P.
PR   22-SEP-2000; 200US-0245667P.
PR   25-SEP-2000; 200US-0249231P.
PR   25-SEP-2000; 200US-0249924P.
PR   25-SEP-2000; 200US-0250078P.
PR   25-SEP-2000; 200US-0250082P.
PR   25-SEP-2000; 200US-0251134P.
PR   25-SEP-2000; 200US-0252080P.
PR   26-SEP-2000; 200US-0235637P.
PR   26-SEP-2000; 200US-0236638P.
PR   27-SEP-2000; 200US-0235711P.
PR   27-SEP-2000; 200US-0235720P.
PR   27-SEP-2000; 200US-0235840P.
PR   27-SEP-2000; 200US-0235863P.

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PR    28-SEP-2000; 2000US-0236028P.
PR    28-SEP-2000; 2000US-0236032P.
PR    28-SEP-2000; 2000US-0236033P.
PR    28-SEP-2000; 2000US-0236034P.
PR    28-SEP-2000; 2000US-0236109P.
PR    28-SEP-2000; 2000US-0236111P.
PR    29-SEP-2000; 2000US-0236842P.
PR    29-SEP-2000; 2000US-0236891P.
PR    02-OCT-2000; 2000US-0237172P.
PR    02-OCT-2000; 2000US-0237173P.
PR    02-OCT-2000; 2000US-0237278P.
PR    02-OCT-2000; 2000US-0237294P.
PR    02-OCT-2000; 2000US-0237295P.
PR    03-OCT-2000; 2000US-0237316P.
PR    03-OCT-2000; 2000US-0237425P.
PR    03-OCT-2000; 2000US-0237598P.
PR    03-OCT-2000; 2000US-0237604P.
PR    03-OCT-2000; 2000US-0237605P.
PR    03-OCT-2000; 2000US-0237606P.
PR    03-OCT-2000; 2000US-0237608P.
PR    01-NOV-2000; 2000US-0244867P.
PR    01-NOV-2000; 2000US-0245084P.
XX
PA    (AVAL-) AVALON PHARM.
XX
PI    Young PB, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI    Soppet DR, Weaver Z;
XX
DR    WPI; 2002-188264/24.
XX
PT    Screening for anti-neoplastic agent involves exposing cells to a chemical
PT    agent to be tested for anti-neoplastic activity, and determining a change
PT    in expression of a gene of a signature gene set.
XX
PS    Claim 1; SEQ ID NO 3116; 44pp; English.
XX
CC    The present invention describes a method (M1) for screening for an anti-
CC    neoplastic agent. The method involves exposing cells to a chemical agent
CC    to be tested for anti-neoplastic activity, determining a change in
CC    expression of at least one gene (I) of a signature gene set, where (I)
CC    comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC    to ABL70110), or is at least 95% identical to (S), where a change in (I)
CC    expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC    activity and can be used in gene therapy. M1 can be used for screening an
CC    anti-neoplastic agent, and can be used for producing a product which is
CC    the data collected with respect to the anti-neoplastic agent as a result
CC    of M1, and the data is sufficient to convey the chemical structure and/or
CC    properties of the agent. M1 can be used in the treatment of cancer such
CC    as colon, breast, lung, thyroid, oesophageal, ovarian, kidney,
CC    prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC    cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC    cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC    tumour
XX
SQ    Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy         1 ACAGTCAGCCGCATGGGCTCCCCGTGCCCAGCCCCTGGCTCCCCCGGCC       60
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        31 ACAGTCAGCCGCATGGGCTCCCCGTGCCCAGCCCCTGGCTCCCCCGGCC       90

Qy        61 CCTGCTCCCAGGGCCTCACTGTGCAACTGCTGCTTCGATGGCCTGTTCCAT      120
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        91 CCTGCTCCCAGGGCCTCACTGTGCAACTGCTGCTTCGATGGCCTGTTCCAT      150

Qy       121 CCCCAGAGGGTTGCCCCGGATGCAGGAGGAATTCCCCGGGGAGCATCCTA      180
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       151 CCCCAGAGGGTTGCCCCGGATGCAGGAGGAATTCCCCGGGGAGCATCCTA      210

Qy       181 GATGACCCACTGGGCGGGAGGAGGAATCTCCCACAGTGAACAGAGGAGGAGGAT      240
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       211 GATGACCCACTGGGCGGGAGGAGGAATCTCCCACAGTGAACAGAGGAGGAGGAT      270

Qy       241 CCACCCCGGAGAGGAGGAATCTACCTTGGAGAGGAGGATCTACCTT      300
             ||||||||||||||||||||||||||||||||||||||||||||||
Db       271 CCACCCGGAGAGGAGGAATCTACCTTGGAGAGGAGGATCTACCTT      330

Qy       301 GAAGTTAAGCCTAAATCAGAAGNAAGAGAGGGCTCCCTGAAGTTAGAGGATCTTACCTACTGTT      360
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       331 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTTACCTACTGTT      390

Qy       361 GAGGCTTCCTGGAGATCTTCAAGAAGACCCCAGAATAAATGCCCACAGGACAAAAGAGGGGAT      420
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       391 GAGGCTTCCTGGAGATCTTCAAGAAGACCCCAGAATAAATGCCCACAGGACAAAAGAGGGGAT      450

Qy       421 GACCAGAGTCATTGGCGCTATGAGAGGGCGCATCCCAGCCTAGAGCTCGTTCTGAGCCTGC      480
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       451 GACCAGAGTCATTGGCGCTATGAGAGGGCGCATCCCAGCCTAGAGCTCGTTCTGAGCCTGC      510

Qy       481 GCGGGGCCGCTTCCAGTCCCCGGTGGAATATCCGCGCCCCCCAGCCCTGCGCCCCCGGCC      540
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       511 GCGGGGCCGCTTCCAGTCCCCGGGATATCCGCGCCCCCAGCCCTGCGCCCCCGGCC      570

Qy       541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCCAGAACTGCCCTGCC      600
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       571 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCCAGAACTGCCCTGCC      630

Qy       601 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTTCCAGCTCCCGCGGCTCCC      660
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       631 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTTCCAGCTCCCGCGGCTCCC      690

Qy       661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCCATCTGCACTGGGGGCTGCAGGTCGTCCGGGC      720
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       691 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCCATCTGCACTGGGGGCTGCAGGTCGTCCGGGC      750

Qy       721 TCCGGAGCACACGTGGAAGGCCACCGTTTCCCTGCCAGGATCCAGGTTCACCTCAGC      780
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       751 TCCGGAGCACACGTGGAAGGCCACCGTTTCCCTGCCAGGATCCAGGTTCACCTCAGC      810

Qy       781 ACCGGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGCGCCGGGGAGGCCTCGGCCGTGTTGGCC      840
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       811 ACCGGCCTTTGCCAGAGTTGACGAGGGCCTTGGGGCGCCGGGGAGGCCTCGGCCGTGTTGGCC      870

Qy       841 GCCTTTCTCGGAGGGGAGGAGAAAACAGTGCCTATGAGCAGTTGCTCTCGGCTTG      900
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       871 GCCTTTCTCGGAGGGGAGGAGAAAACAGTGCCTATGAGCAGTTGCTCTCGGCTTG      930

Qy       901 GAAGAAAATCGCTGAGGAAGGTCTCAGAGAGCTCAGGTCCCAGGACTGGACATATCTGCACTC      960
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       931 GAAGAAAATCGCTGAGGAAGGTCTCAGAGAGCTCAGGTCCCAGGACTGGACATATCTGCACTC      990

Qy       961 CTGCCCCTCGACTTCAGCGGCTTCAGCTTCCAAATATGAGGGGTCTCCTGACTACACCGCC      1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       991 CTGCCCCTCGACTTCAGCGGCTTCAGCTTCCAAATATGAGGGGTCTCCTGACTACACCGCCTGT      1050

Qy      1021 GCCCAGGGGTCGTCATCTGGACTGGTTTAACCAGACAGTGACTGCTAAGCACGTC      1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1051 GCCCAGGGGTCGTCATCTGGACTGGTTTAACCAGACAGTGACTGCTAAGCACGTC      1110

Qy      1081 CACACCCTTCTGACACCCTGTGGGGACCTGACTCGGGTGACTGAACTTCCGA      1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1111 CACACCCTTCTGACACCCTGTGGGGACCTGACTCGGGTGACTGAACTTCCGA      1170

Qy      1141 GCGACGCAGCCTTTGAATGGGCGGAGTGATTGAGGCCTTCCCTGGACTTGCAGC      1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1171 GCGACGCAGCCTTTGAATGGGCGGAGTGATTGAGGCCTTCCCTGGACTTGCAGC      1230

Qy      1201 AGTCCTCGGGCGTCGGCCAGTCCAGCTGAATTCCTGGCCTGGGTGACATCCTA      1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1231 AGTCCTCGGGCGTCGGCCAGTCCAGCTGAATTCCTGGCCTGGGTGACATCCTA      1290

Qy      1261 GCCCTGGTTTTGGGCCTCCTTTTTGCTGGTTCACCAGGGTGGGTTCAGATGAGA      1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1291 GCCCTGGTTTTTGGGCCTCCTTTTTGCTGGTTCACCAGGGTGGGTTCAGATGAGA      1350
```

Qy 1321 AGGCAGCACAGGAAGGGGAGGAACCAAAAGGGGGGGTGAGGCTACCGCGCCCAGCAGCAGGAGGGTAGCCGAG 1380
         |||||||||||||||||||| |||||||||||||||||| |||||||||||||||||| |||||||||||||||
Db 1351 AGGCAGCACAGGAAGGGGAACCAAAAGGGGGGGTGAGCTACCGCGCCCAGCAGAGGGTAGCCGAG 1410

Qy 1381 ACTGGAGGCCTAGAGGCTGGATCTTGGAGAATGTCAGAAGACCCAGCCCCAGCAGGGCCATCTGAGGG 1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1411 ACTGGAGGCCTAGAGGCTGGATCTTGGAGAATGTCGAGAAGACCCAGCCCCAGCAGGGCCATCTGAGGG 1470

Qy 1441 GGAGCCCGTAACTGTCCTGTCCTGCTCATTATCCCACTTCCTTTTAACTGCCAAGAAATT 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1471 GGAGCCCGTAACTGTCCTGTCCTGCTCATTATCGCCACTTCCTTTTTAACTGCCAAGAAATT 1530

Qy 1501 TTTTAAAATAAAATATTTTATAAT 1522
         ||||||||||||||||||||||||
Db 1531 TTTTAAAATAAAATATTTTATAAT 1552

RESULT 7
ABL62179

ID   ABL62179 standard; DNA; 1552 BP.
XX
AC   ABL62179;
XX
DT   15-MAY-2002 (first entry)
XX
DE   Colon adenocarcinoma related gene sequence SEQ ID NO:516.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; db.
XX
OS   Homo sapiens.
XX
XX
PF   30-MAY-2001; 2001WO-US010838.
PD   13-DEC-2001.
XX
PN   WO20019462-A2.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
PA   (AVAL-) AVALON PHARM.
XX
DR   WPI; 2002-188264/24.
XX
PT   The present invention describes a method (M1) for screening for an anti-
PT   neoplastic agent. The method involves exposing cells to a chemical agent
PT   to be tested for anti-neoplastic activity, determining a change in
PT   expression of at least one gene (I) from a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match   100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ACAGTCAGCGCGCATCGGCTCCCCGTGCCCCCAGCCCCTCCCTCTGTTGATCCCGGCC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 ACAGTCAGCGCGCATGGCTCCCCGTGCCCCCAGCCCCTCCCTCTGTTGATCCCGGCC 90

Qy   61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCGTGCTTCTGATGCTCCAT 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91 CCTGCTCCAGGCCTTCACTGTGCAACTGCTGCTGCTTCGTCACTGCTGCTTCGTCCGTGTCCCAT 150

Qy 121 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 151 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 210

Qy 181 GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGAGGATTCACCCAGAGAGGAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 211 GATGACCCACTGGGCGCGAGGAGGATCTGCCCAGTGAAGAGAGGATTCACCCAGAGAGGAT 270

Qy 241 CCACCCGGAGAGGAGGATCTTACCTTGGAGGAGGAGGATCTACCT 300
        |||||||||||||||||||||||||||||||||||||||||||||
Db 271 CCACCCGGAGAGGAGGATCTTACCTTGGAGGAGGAGGATCTACCT 330

Qy 301 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGGCTCCCTGAAGTTAAGACGGATCTTACCTACTGTT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 331 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGGCTCCCTGAAGTTAAGAGGATCTTACCTACTGTT 390

Qy 361 GAGGCTCCTGGAGATCCTCAAGGACCCCAGAATAATGCCCACGGGACAAAGAAGAGGGGAT 420

```
Db    391 GAGGCTTCCTGGAGAGATCCTCAAGAACCCAGGAATAATGCCCACAGGGACACAGGAAGGGGGAT 450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    391 GAGGCTTCCTGGAGAGATCCTCAAGAACCCAGGAATAATGCCCACAGGGACACAGGAAGGGGGAT 450

Db    421 GACCAGAGTCATTGGCGCTATGGAGGGGACACCCGCCTTGGCCCTGCCCCGGGGTGTCCCAGCCTGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421 GACCAGAGTCATTGGCGCTATGGAGGGGACACCCGCCTTGGCCCTGCCCCGGGGTGTCCCAGCCTGC 480

Db    451 GACCAGAGTCATTGGCGCTATGGAGGGCGACCCCGCCCCGGGGTGTCCCCAGCCTGC 510
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    451 GACCAGAGTCATTGGCGCTATGGAGGGCGACCCCGCCCCGGGGTGTCCCCAGCCTGC 510

Db    481 GCGGGGCCGGCTTCCAGTCCCCGGGTGGATATCCGGCCCCCCCCAGCTCGCCGCCTTTCTCCCGGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481 GCGGGGCCGGCTTCCAGTCCCCGGGTGGATATCCGGCCCCCCCCAGCTCGCCGCCTTTCTCCCGGCC 540

Db    511 GCGGGGGCCGGCTTCCAGTCCCCGGGTGGGATATCCGGCCCCCCCCAGCTCGCCGCCTTCTGCCCGGCC 570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    511 GCGGGGGCCGGCTTCCAGTCCCCGGGTGGGATATCCGGCCCCCCCCAGCTCGCCGCCTTCTGCCCGGCC 570

Db    541 CTGCGGCCCCCTGGGAACTCCTGGGCGTTCCAGCTCCCGGCCGCTCCCAGAACTGCGCCGCCTGGCC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541 CTGCGGCCCCCTGGGAACTCCTGGGCGTTCCAGCTCCCGGCCGCTCCCAGAACTGCGCCGCCTGGCC 600

Db    571 CTGCGGAGCACACTGGGGAACTCCTGGGCTTCAGCTCCCGCGCTCCCAGGAACTGCGGCCGCTGGGC 630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    571 CTGCGGAGCACACTGGGGAACTCCTGGGCTTCAGCTCCCGCGCTCCCAGGAACTGCGGCCGCTGGGC 630

Db    601 AACAATGGCCACAGTGTGCAACTGACACCCGCCTTCTCCTGGGCTAGAGATGGCTCTGGGGTCCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601 AACAATGGCCACAGTGTGCAACTGACACCCGCCTTCTCCTGGGCTAGAGATGGCTCTGGGGTCCC 660

Db    631 GGGCGGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTCGGGGC 690
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    631 GGGCGGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTCGGGGC 690

Db    661 GGGCGGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTTCGGGGC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661 GGGCGGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGGCTGCAGGTCGTTCGGGGC 720

Db    691 GGGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCGAGGTCGTCGCTCGGGC 750
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    691 GGGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCGAGGTCGTCGCTCGGGC 750

Db    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCACGTGGTTCACCTCAGC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCACGTGGTTCACCTCAGC 780

Db    751 TCGGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCCTCAGC 810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    751 TCGGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCCTCAGC 810

Db    781 ACCGCCTTTGCCACAGAGTTGACAGAGGCCTTGGGGCCGGCCTTGGGCCGGGGGAGGCCGGGCCGGTCCTGTTCGGCC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 ACCGCCTTTGCCACAGAGTTGACAGAGGCCTTGGGGCCGGCCTTGGGCCGGGGGAGGCCGGGCCGGTCCTGTTCGGCC 840

Db    811 ACCGGCCTTTGCCACAGTTGACAGAGGCCTTGCCGGCCGGGCCGGGGGAGGCCCTTGGGCCGGGTTGGCC 870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    811 ACCGGCCTTTGCCACAGTTGACAGAGGCCTTGCCGGCCGGGCCGGGGGAGGCCCTTGGGCCGGGTTGGCC 870

Db    841 GCCTTTTCTGGAGGAGGGGCCGGAAGAAAACAGTGCCTATGAGCAGAGTTGCGTCGTGTCTCGGCTTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 GCCTTTTCTGGAGGAGGGGCCGGAAGAAAACAGTGCCTATGAGCAGAGTTGCGTCGTGTCTCGGCTTG 900

Db    871 GCCTTTTCTCGGGGAGGAGGGCCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCGTCTCTCGGCTTG 930
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    871 GCCTTTTCTCGGGGAGGAGGGCCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCGTCTCTCGGCTTG 930

Db    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACAGGACATATCTGCACTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACAGGACATATCTGCACTC 960

Db    931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAAGGACTGGACATATCTGCACTC 990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAAGGACTGGACATATCTGCACTC 990

Db    961 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATTATGAGGGGGTTCTCTGACTACACGCCCCTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATTATGAGGGGGTTCTCTGACTACACGCCCCTGT 1020

Db    991 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATTATGAGGGGGTTCTCTGACTACACGCCCTGT 1050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    991 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATTATGAGGGGGTTCTCTGACTACACGCCCTGT 1050

Db   1021 GCCCAGGGGTGTCATCTCGAGGACTGTGTTTAACCAGACAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021 GCCCAGGGGTGTCATCTCGAGGACTGTGTTTAACCAGACAGTGCTAAGCAGCTC 1080

Db   1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGCGTCTGAGCAGGCTC 1110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGCGTCTGAGCAGGCTC 1110

Db   1081 CACACCCTCTCTGACACCCGTGGGGACCTGGCTACAGCTGAACTTCCGA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081 CACACCCTCTCTGACACCCGTGGGGACCTGGCTACAGCTGAACTTCCGA 1140

Db   1111 CACACCCTTCTCTGACACCCGTGGGACCTGGTCGTGAACTTCCGA 1170
          |||||||||||||||||||||||||||||||||||||||||||
Qy   1111 CACACCCTTCTCTGACACCCGTGGGACCTGGTCGTGAACTTCCGA 1170

Db   1141 GCCGACGCAGCCCTTTGAATGGGGGCCAGTCGTACGGTACCGGCGCTAGCGCAGC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 GCCGACGCAGCCCTTTGAATGGGGGCCAGTCGTACGGTACCGGCGCTAGCGCAGC 1200

Db   1171 GCCGACGCAGCCCTTGAATGGGGCCAGTCGTACGGTACCGGCGCTAGCGGACAGC 1230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1171 GCCGACGCAGCCCTTGAATGGGGCCAGTCGTACGGTACCGGCGCTAGCGGACAGC 1230

Db   1201 AGTCCTCGGGCTGCGGCCAGTCCACGTCCGACTGAATTCCTGCCTGGCGTGGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201 AGTCCTCGGGCTGCGGCCAGTCCACGTCCGACTGAATTCCTGCCTGGCGTGGGTGACATCCTA 1260

Db   1231 AGTCCTCGGGGCTGCTGAGGCCAGTCCACTGAATTCCTGCCTGGCGTGGGTGACATCCTA 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1231 AGTCCTCGGGGCTGCTGAGGCCAGTCCACTGAATTCCTGCCTGGCGTGGGTGACATCCTA 1290

Db   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGGTCCGTGTCGTGTCGCAGATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGGTCCGTGTCGTGTCGCAGATGAGA 1320

Db   1291 GCCCTGGTTTTTGGCCTTCCTTTTTGCTGTCACCAGCGCGTTCCTTGTGTCACGAGGATGAGA 1350
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1291 GCCCTGGTTTTTGGCCTTCCTTTTTGCTGTCACCAGCGCGTTCCTTGTGTCACGAGGATGAGA 1350

Db   1321 AGGCAGCACAGGAGGAACCAAAAGGGGTGTGAGCTACCGGACGTCGAGGTAGCCGAG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 AGGCAGCACAGGAGGAACCAAAAGGGGTGTGAGCTACCGGACGTCGAGGTAGCCGAG 1380

Db   1351 AGGCAGCACAGAGGGGGGAACCAAAAGGGGTGTGAGCTACCGGACGTAGCCGAG 1410
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1351 AGGCAGCACAGAGGGGGGAACCAAAAGGGGTGTGAGCTACCGGACGTAGCCGAG 1410

Db   1381 ACTGGAGAGCCTAGAGGCTGGACTTTGGGAGAAGTGTGAGGAAGGCCATCGAGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381 ACTGGAGAGCCTAGAGGCTGGACTTTGGGAGAAGTGTGAGGAAGGCCATCGAGGG 1440

Db   1411 ACTGGAGCCCTAGAGGCTGGATCTTGAGAAAGTGAGAAGCAGCCAGAGGGCATCTGAGGG 1470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1411 ACTGGAGCCCTAGAGGCTGGATCTTGAGAAAGTGAGAAGCAGCCAGAGGGCATCTGAGGG 1470

Db   1441 GGAGCCGGTAACTGTCCTGCTGTCATTATGCCACTTCCTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441 GGAGCCGGTAACTGTCCTGCTGTCATTATGCCACTTCCTTTAACTGCCAAGAAATT 1500

Db   1471 GGAGCCGGTAACTGTCCTGCTGGTGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT 1530
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501 TTTTAAATTAAAATATTTATAAT 1522
          |||||||||||||||||||||||
Db   1531 TTTTAAATTAAAATATTTATAAT 1552
```

RESULT 8

ABL65416

ID   ABL65416 standard; DNA; 1552 BP.
XX
AC   ABL65416;
XX
DT   15-MAY-2002 (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:3753.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   22-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235337P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   03-OCT-2000; 2000US-0237316P.
PR   03-OCT-2000; 2000US-0237425P.
PR   03-OCT-2000; 2000US-0237598P.
PR   03-OCT-2000; 2000US-0237604P.
PR   03-OCT-2000; 2000US-0237606P.
PR   03-OCT-2000; 2000US-0237608P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX

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PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene of a signature gene set.
XX
PS   Claim 1; SEQ ID NO 3753; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match              100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity    100.0%;
Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ACAGTCAGCGCATGGCTCCCGTGCCCCAGCCCCTGTCCTGTTGATCCGGCC 60
Db     31 ACAGTCAGCGCATGGCTCCCGTGCCCCAGCCCCTGTCCTGTTGATCCGGCC 90

Qy     61 CCTGCTCCAGGCGCTCACTGCTGCGTCGTCACTGCTGCTTCTGATGCCTGT 120
Db    151 CCTGCTCCAGGCGCTCACTGCTGCGTCGTCACTGCTGCTTCTGATGCCTGT 150

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGAA 180
Db    181 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGAA 180

Qy    181 GATGAACCCACTGGGCGGAGGAGTCGCCCAGTGAAGAGGAGGAGGAGGAT 240
Db    211 GATGAACCCACTGGGCGGAGGAGTCGCCCAGTGAAGAGGAGGAGGAGGAT 270

Qy    241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 300
Db    271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAAATCAGGAAGAAGAAGGCTCCCTGAAGTTAGGATCTTACCTACTCGTT 360
Db    331 GAAGTTAAGCCTAAAATCAGGAAGAAGAAGGCTCCCTGAAGTTAGGATCTTACCTACTCGTT 390

Qy    361 GAGGCTCCTGGGAGATCCTCAAGAAACCCAGAAATAAGTGCCCACAGGGACAAAGAAGGGGAT 420
Db    391 GAGGCTCCTGGGAGATCCTCAAGAAACCCAGAAATAAGTGCCCACAGGGACAAAGAAGGGGAT 450

Qy    421 GACCAGAGTCATTGGCGTATGGAGGCGGACCCGCGCCCTTGGCCCTGGTGTCCCCAGCCTGC 480
Db    451 GACCAGAGTCATTGGCGTATGGAGGCGGACCCGCGCCCTTGGCCCTGGTGTCCCCAGCCTGC 510

Qy    481 GCGGGGCCGCTTCCAGTCCCCGGGTGGATAATCCGCGCGCGCTCGCGCGCCCGGGTGGGCC 540
Db    511 GCGGGGCCGCTTCCAGTCCCCGGGTGGATAATCCGCGCGCGCTCGCGCGCCCGGGTGGGCC 570

Qy    541 CTGCGCCCCCTTGGGAACTCCTTGGGGCTTCCAGCTTCCAGAACTGCGGC 600
Db    571 CTGCGCCCCCTTGGGAACTCCTTGGGGCTTCCAGCTTCCAGAACTGCGGC 630

Qy    601 AACAATGGCCACACAGTGTGCAACTGACCCGGCCTTCCAGCTCCCAGAGAGGATGGCCCTGCGC 660
Db    631 AACAATGGCCACACAGTGTGCAACTGACCCGGCCTTCCAGCTCCCAGAGAGGATGGCCCTGCGC 690

Qy    661 GGGCGGGGAGTACCGGCGGCTTCGCAGTCGCATCTGCACTGCAGCTGCACTGGGAGGTCGTCGGGGC 720
Db    691 GGGCGGGGAGTACCGGCGGCTTCGCAGTCGCATCTGCACTGCAGCTGCACTGGGAGGTCGTCGGGGC 750

Qy    721 TCGGAGCACACTGTGGAAGGCCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCTCAGC 780
Db    751 TCGGAGCACACTGTGGAAGGCCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCTCAGC 810

Qy    781 ACCGGCCTTTGCCCAGAGTTGACGGAGGCCCACCGTTTGGGGCCGGAGGCCCTTGGGGCC 840
Db    811 ACCGGCCTTTGCCCAGAGTTGACGGAGGCCCACCGTTTGGGGCCGGAGGCCCTTGGGGCC 870

Qy    841 GCCTTTCTTGGAGGAGGGCCCGGAGAGAAAAACAGTGCCTATGAGCAGTTGCGTGTCTCGGCTTG 900
Db    871 GCCTTTCTTGGAGGAGGGCCCGGAGAGAAAAACAGTGCCTATGAGCAGTTGCGTGTCTCGGCTTG 930

Qy    901 GAAGAAAATCGGCTGAGGAAGGCTCAGGACTCAGGTGGCCTATGAGCAGTTGCGTCTCGGCTTG 960
Db    931 GAAGAAAATCGGCTGAGGAAGGCTCAGGACTCAGGTGGCCTATGAGCAGTTGCGTCTCGGCTTG 990

Qy    961 CTGCCCCTCTGACTTCAGCCGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGGCCCCTGT 1020
Db    991 CTGCCCCTCTGACTTCAGCCGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGGCCCCTGT 1050

Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
Db   1051 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1110

Qy   1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140
Db   1111 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1170

Qy   1141 GCGACGCAGCCTTTGAAATGGGCGGAGTGATTGAGGGCCTCTTCCCTGGGGCTGGACAGC 1200
Db   1171 GCGACGCAGCCTTTGAAATGGGCGGAGTGATTGAGGGCCTCTTCCCTGGGGCTGGACAGC 1230

Qy   1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCGTGGTGGTGGACAGC 1260
Db   1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCGTGGTGGTGGACAGC 1290

Qy   1261 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGCGTGCGGTGCGTTCCTTGTCAGATGGA 1320
Db   1291 GCCCTGGTTTTGGCCTCCTTTTTGCTGTCACCAGCGTGCGGTGCGTTCCTTGTCAGATGGA 1350

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTGAGCTACCGCCCAGCGAGGTAGCCGAG 1380
Db   1351 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTGAGCTACCGCCCAGCGAGGTAGCCGAG 1410

Qy   1381 ACTGGAGGCCTTAGAGGCCTGGACTCTTGGAGAATGTGAGAAGCCAGCATCTGAGGG 1440
Db   1411 ACTGGAGGCCTTAGAGGCCTGGACTCTTGGAGAATGTGAGAAGCCAGCATCTGAGGG 1470

Qy   1441 GGAGCCCGGTAACTGTCCCGCTCATTATGCCAACTTCCTTTTAAACTGCCAAGAAATT 1500
Db   1471 GGAGCCCGGTAACTGTCCCGCTCATTATGCCAACTTCCTTTTAAACTGCCAAGAAATT 1530

Qy   1501 GGAGCGGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTAAACTGCCAAGAAATT 1530
Db   1531 TTTTAAAATAAATATTTATAAT 1552

Qy   1531 TTTTAAAATAAATATTTATAAT 1552
Db   1531 TTTTAAAATAAATATTTATAAT 1552
```

RESULT 9
ABL68346
ID   ABL68346 standard; DNA; 1552 BP.
XX

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AC   ABL68346;
XX
DT   15-MAY-2002 (first entry)
XX
DE   Kidney cancer related gene sequence SEQ ID NO:6683.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   25-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   26-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236024P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
PR   02-OCT-2000; 2000US-0237173P.
PR   02-OCT-2000; 2000US-0237278P.
PR   02-OCT-2000; 2000US-0237294P.
PR   02-OCT-2000; 2000US-0237295P.
PR   02-OCT-2000; 2000US-0237316P.
PR   03-OCT-2000; 2000US-0237425P.
PR   03-OCT-2000; 2000US-0237598P.
PR   03-OCT-2000; 2000US-0237604P.
PR   03-OCT-2000; 2000US-0237606P.
PR   03-OCT-2000; 2000US-0237600P.
PR   01-NOV-2000; 2000US-0244867P.
PR   01-NOV-2000; 2000US-0245084P.
XX
XX
PA   (AVAL-) AVALON PHARM.
XX
PI   Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI   Soppet DR, Weaver Z;
XX
DR   WPI; 2002-188264/24.
XX
PT   Screening for anti-neoplastic agent involves exposing cells to a chemical
PT   agent to be tested for anti-neoplastic activity, and determining a change
PT   in expression of a gene of a signature gene set.
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PS   Claim 1; SEQ ID NO 6683; 44pp; English.
XX
CC   The present invention describes a method (M1) for screening for an anti-
CC   neoplastic agent. The method involves exposing cells to a chemical agent
CC   to be tested for anti-neoplastic activity, determining a change in
CC   expression of at least one gene (I) of a signature gene set, where (I)
CC   comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC   to ABL70110), or is at least 95% identical to (S), where a change in
CC   expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC   activity and can be used in gene therapy. M1 can be used for screening an
CC   anti-neoplastic agent, and can be used for producing a product which is
CC   the data collected with respect to the anti-neoplastic agent as a result
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1522;  DB 6;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAGTCAGCCGCATGGCTCCCCTTGTGCCCCCAGCCCCTTGGCTTCCCTCTGTTGATCCCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ACAGTCAGCCGCATGGCTCCCCTTGTGCCCCCAGCCCCTTGGCTTCCCTCTGTTGATCCCCGGCC 90

Qy         61 CCTGGCTCCAGGCGCCTCACTGTGCAACTGCTGCTTCACTGCCGCTTCGATGCCTGTCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CCTGGCTCCAGGCGCCTCACTGTGCAACTGCTGCTTCACTGCCGCTTCGATGCCTGTCCAT 150

Qy        121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCTTGGGAGGAGGGTCTTCTGGGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 CCCCAGGAGGTTGCCCCGGATGCAGGAGGAGATTCCCCTTGGGAGGAGGGTCTTCTGGGAA 210

Qy        181 GATGAGCCACTGGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GATGAGCCACTGGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 270

Qy        241 CCACCCGGAGAGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGATCTACCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGATCTACCT 330

Qy        301 GAAGTTAAGCCTAAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GAAGTTAAGCCTAAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 390

Qy        361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCCACAGGAGAAGAAGAGGGGAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCCACAGGAGAAGAAGAGGGGAT 450

Qy        421 GACCAGAGTCATTGGCGCTATGGAGGCGACCACGGGTGTCCCCGGAGCTGCTGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GACCAGAGTCATTGGCGCTATGGAGGCGACCACGGGTGTCCCCGGAGCTGCTGC 510

Qy        481 GCGGGCGCGCCTTCCAGTCCCCGGTGGATATCCGGCCCCCCCAGCTGCCGCCTTCTGCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GCGGGCGCGCCTTCCAGTCCCCGGTGGATATCCGGCCCCCCCAGCTGCCGCCTTCTGCC 570

Qy        541 CTGCGCCCCCTGAACTCCCTGGGCTTCCAGCTGCCCTGCGCCCTGCGCC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTGCGCCCCCTGAACTCCCTGGGCTTCCAGCTGCCCTGCGCCCTGCGCC 630

Qy        601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCTCCTGGGCTTAGAGATGGGCTCCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCTCCTGGGCTTAGAGATGGGCTCCC 690

Qy        661 GGGCGCGGGAGTACCGGGCGTCTGCGAGCTCCATCTGCACTGGGGGGCTGCAGGTCGTTCCGGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GGGCGCGGGAGTACCGGGCGTCTGCGAGCTCCATCTGCACTGGGGGGCTGCAGGTCGTTCCGGC 750
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Qy    721 TCCGAGCACACTGTGGAAGGGCCACACGGTTCCCTGCCGAGATCCACGTCGGTTCACCTCAGC    780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCCGAGCACACTGTGGAAGGGCCACACGGTTCCCTGCCGAGATCCACGTCGGTTCACCTCAGC    810

Qy    781 ACCGCCCTTGCCAAGTTGACGAGTTGACGAGGCCTTGGGGGCCCCCGGAGGCCTGGGCCGTGGCC    840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ACCGCCCTTGCCAAGTTGACGAGTTGACGAGGCCTTGGGGGCCCCCGGAGGCCTGGGCCGTGGCC    870

Qy    841 GCCTTTCTCTGGAGGAGGGCCGGGAAGAAAACAGTGCCCCTATGAGCAGTTGCTGTTCTGCTTG    900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTCTTGGAGGAGGGGCCCGGAAGAAAACAGTGCCCTATGAGCAGTTGCTGTTCTGCTTG    930

Qy    901 GAAGAAAATCGGCTGAGGAAGGGCTCAGAGACTCAGGTCCCCAGGGACTGGGACACATATCTGCACTC    960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 GAAGAAAATCGGCTGAGGAAGGGCTCAGAGACTCAGGTCCCCAGGGACTGGGACACATATCTGCACTC    990

Qy    961 CTGCCCTGACTTCAGCCGCTCACTTCCAATATGAGGGGGTCTCTGACTACACCGCCCCTGT   1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGCCCCTGT   1050

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTTAACCAGACAGTGATGATGATGTGAGTGCTAAGCAGCTC   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GCCCAGGGGTGTCATCTGGACTGTGTTTTAACCAGACAGTGATGATGATGTGAGTGCTAAGCAGCTC   1110

Qy   1081 CACACCCCTTCTCGACACCCGTGTGGGGACCTGGTCGGCTACAGCTGAACTTCCGA   1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 CACACCCCTTCTCGACACCCGTGTGGGGACCTGGTCGGCTACAGCTGAACTTCCGA   1170

Qy   1141 GCGACGCAGCCCTTGAATGGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGTGGTGGACAGC   1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGTGGTGGACAGC   1230

Qy   1201 AGTCCTCGGGCTCGCTGACCCAGTCCAGTGAATTCCTGCCTGGCTGCTGCTGGTGACATCCTA   1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 AGTCCTCGGGCTCGCTGACCCAGTCCAGTGAATTCCTGCCTGGCTGCTGCTGGTGACATCCTA   1290

Qy   1261 GCCCTGGTTTTTGGCCTCTCCTTTTTGGCTGTCAGGTCGCGGGTTCCTTGTGTCAGATGAGA   1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 GCCCTGGTTTTTGGCCTCTCTTTTTTGGCTGTCACCAGGTCGCGGGTTCCTTGTGCAGATGAGA   1350

Qy   1321 AGGCAGCAGGAGGGGGAACCAAAGGGGGTGTGAGCTACCGCCAGGAGGTAGCCGAG   1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AGGCAGCAGGAGGGGGAACCAAAGGGGGTGTGAGCTACCGCCAGGAGGTAGCCGAG   1410

Qy   1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCCATCTCGAGGG   1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGCATCTGAGGG   1470

Qy   1441 GGAGCCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT   1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471 GGAGCCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT   1530

Qy   1501 TTTTAAAATAAATATTTATAAT   1522
          ||||||||||||||||||||||
Db   1531 TTTTAAAATAAATATTTATAAT   1552
```

```
PS   Detecting a lung cancer-associated transcript in a cell from a patient
     for treating lung cancer, by contacting a biological sample from the
     patient with a polynucleotide that exhibits increased or decreased
     expression in lung cancer.
XX
CC   The invention relates to a method for detecting a lung cancer-associated
CC   transcript in a cell from a patient, comprising contacting a biological
CC   sample from the patient with a polynucleotide that selectively hybridises
CC   to a sequence that is at least 80 % identical to a gene that exhibits
CC   increased or decreased expression in lung cancer samples. Lung cancer-
CC   associated polynucleotides and polypeptides are used for identifying a
CC   compound that modulates a lung cancer-associated polypeptide, for
CC   inhibiting proliferation of a lung cancer-associated cell to treat lung
CC   cancer in a patient and for treating a mammal having lung cancer by
CC   administering a modulatory compound identified. The methods are useful
CC   for treating lung cancer or other benign or precancerous lesions, e.g.
CC   lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC   lung cancer, such as small cell lung cancer, non-small cell
CC   emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC   hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC   bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC   for diagnostic purposes and as targets for screening for therapeutic
CC   compounds that modulate lung cancer, such as antibodies. Sequences
CC   ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC   invention
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
```

```
Query Match        100.0%;  Score 1522;  DB 8;  Length 1552;
Best Local Similarity   100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 ACAGTCAGCGCATGGCTCCCCTGTGCCCCAGCGCCCTGGCCTTCCCCTTCGTTGATCCCGGCC    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTCAGCGCATGGCTCCCCTGTGCCCCAGCGCCCTGGCCTTCCCCTTCGTTGATCCCGGCC    90

Qy     61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGCTGGTGTCACTCGCTTCGATGGCCTGTCCAT   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGCTGGTGTCACTCGCTTCGATGGCCTGTCCAT   150

Qy    121 CCCCAGAGGTTGCCCCGGACTGCAGGAGGATTCCCCCTTGGGAGGAGGAGGGCTCTTCGGGGAA   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 CCCCAGAGGTTGCCCCGGACTGCAGGAGGATTCCCCCTTGGGAGGAGGAGGGCTCTTCGGGGAA   210

Qy    181 GATGACCCACTGGGCGGAGGATCTGCCCAGTGAAGAGGAGATTCACCCAGAGGAGGAGGAT   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGGAGGATCTGCCCAGTGAAGAGGAGATTCACCCAGAGGAGGAGGAT   270

Qy    241 CCACCCCGGAGGAGGAGGAGGAGGGATCTACCTGGAGGAGGAGGATCTACCT   300
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Qy          271 CCACCCGGAGGAGGAGGGATCTACCTGAGAGGAGGATCTACCTT 330
                ||||||||||||||||||||||||||||||||||||||||||||
Db         1351 AGGCAGCACAGAAGGAGGGAACCAAAGGGGGGTGGTGAGCTACCGGCCCAGCAGGAGGTAGCCGAG 1410

Qy          301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 ACTGGAGCCTAGAGGGCTGGATCTTGGAGAATGTGGAGAAGCCAGCCAGCCAGGGCATCTGAGGG 1440

Qy          331 GAAGTTAGCCTAAATCAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1411 ACTGGAGCCTGAGAGGGCTGGATCTTGGGAGAATGTGAGAAGCCAGCCGAGGGCATCTGAGGG 1470

Qy          361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAGAATAAATGCCCACAGAAGGAGGGGAT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 GGAGCGGGGTAACTGTCTCCTGTTCTGCTCAGTTATGGCCACTTCCTTTAACTGCCAGAAATT 1500

Qy          391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAGAATAATGCCCCACAGGGACAAAAGAAAGGGGAT 450
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1471 GGAGCCGGTAACTGTCCGTTCGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT 1530

Qy          421 GACCAGAGTCATTGGCGCTATGCGATGGGAGGGGCGACCCCGGCCCCGGGGTGTCCCCAGCCTGC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1501 TTTTAAAATTAAATATTTTATAAT 1522

Qy          451 GACCAGAGTCATTGGCGCTATGGGAGGGGCGACCCCGGCCCCGGGGTGTCCCCAGCCTGC 510
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1531 TTTTAAAATTAAATATTTTATAAT 1552

Qy          481 GCGGGGCGGCGCTTCCAGTCCCCGGGTGGGATATCCGGCCCCCGCCCAGCTCGCGGCCTTCGCCGGCC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          511 GCGGGGCGGCGCTTCCAGTCCCCGGGTGGGATATCCGGCCCCCGCCCAGCTCGCGGCCTTCTCCCCGCC 570

Qy          541 CTGGCGCCCCCTGGGAACTCCTGGGCTTCAGCTGCCCCGGAACTGCCCTGCCC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          571 CTGGCGCCCCCTGGGAACTCCTGGGCTTCAGCTGCCCCGGAACTGCGCGCTGCCC 630

Qy          601 AACAATGCCACAGTGTGCAATGACCCTGCCTCCTGGGTGGGCTAGAGATGGCTCTGGGGTCCC 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          631 AACAATGGCCACAGTGTGCAAGTGACCCTGCCTCCTGGGTGGGCTAGAGATGGCTCTGGGGTCCC 690

Qy          661 GGGCGGGGAGGTACCGGGGCTCTCGACTCTCGACACTGGGGGGGGGCTGCGAGGTGTCTCCGGGC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 GGGCGGGGAGGTACCGGGGCTCTCGACTCTCGACACTGGGGGGGGGCTGCGAGGTGTCTCCGGGC 720

Qy          691 GGGCGGGGAGTACCCGGGCCTCTGCAGCCTGCATCTCGCAGCTGCAGGTCGTCCCGGGC 750
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          721 TCGGAGCACACTGTGGAAGCCACCGTTCCCTGCCGAGATCCAGCGTGGTTCACCTCAGC 780

Qy          721 TCGGAGCACACTGTGGAAGCCACCGTTCCCTGCCGAGATCCAGCGTGGTTCACCTCAGC 780

Db          751 TCGGAGCACACTGTGGAAGCCACCGTTCCCTGCCGAGATCCAGCGTGGTTCACCTCAGC 810

Qy          751 TCGGAGCACACTGTGGAAGCCACCGTTCCCTGCCGAGATCCAGCGTGGTTCACCTCAGC 810

Qy          781 ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCTGGCCGGTTGTTGGGCC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCGCCCTGCCCGGTTGTTGGGCC 840

Qy          811 ACCGGCTTTTGCCCAGAGTTGACGAGGCCCTGGCCGGTTGTTGGGCC 870
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          811 ACCGGCTTTTGCCCAGAGTTGACGAGGCCCTGGCCGGTTGTTGGGCC 870

Qy          841 GCCTTTCTGGGAGGGGAAAGCAGAGTGCCTATGAGCAGTTGCTGCTGTCTCCGGTTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 GCCTTTCTGGGAGGGGAAAGCAGAGTGCCTATGAGCAGTTGCTGCTGTCTCCGGTTG 900

Qy          871 GCCTTTCTTGGAGGAGGGGGCCCGGGAAGAAAACAGTGCCTATGACCAGTTGCTTCCGGTTG 930
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          871 GCCTTTCTTGGAGGAGGGGGCCCGGGAAGAAAACAGTGCCTATGACCAGTTGCTTCCGGTTG 930

Qy          901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Qy          931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990

Qy          961 CTGCCCTTCTGACTTGAGCCGTACTCTTCGACTACACCGCCCGTT 1020
                ||||||||||||||||||||||||||||||||||||||||||||
Db          961 CTGCCCTTCTGACTTGAGCCGTACTCTTCGACTACACCGCCCGTT 1020

Qy          991 CTGCCCTTCTGACTTGAGCCGCTACTTCCAAATATGGAGGGGTCTCTGACTTACACCCCCTGT 1050
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          991 CTGCCCTTCTGACTTGAGCCGCTACTTCCAAATATGGAGGGGTCTCTGACTTACACCCCCTGT 1050

Qy         1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACTGATGTGCTAAGCCAGCTC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACACTGATGTGCTAAGCCAGCTC 1080

Qy         1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTGAGTGGCTAAGCACTC 1110
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1051 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTGAGTGGCTAAGCACTC 1110

Qy         1081 CACACCCTTCTGACACCCTGTGGGGACCTGGTCGTGACTCTGGGTCTACAGCTGAACTTCCGA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 CACACCCTTCTGACACCCTGTGGGGACCTGGTCGTGACTCTGGGTCTACAGCTGAACTTCCGA 1140

Qy         1111 CACACCCTTCTCTGACACCCGTGTGACTCTGCGCTCAGCTGAACTTCCGA 1170
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1111 CACACCCTTCTCTGACACCCGTGTGACTCTGCGCTCAGCTGAACTTCCGA 1170

Qy         1141 GCGACGCAGCCTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCGGAGTGGACAGC 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 GCGACGCAGCCTTGAATGGGCCAGTGATTGAGGCCTCCTTCCCGTTGCTGGTGGACAGC 1200

Qy         1171 GCCACGCAGCCTTTGAATGGGCCAGTGATTGAGGGCTCCTTCCCGTTGCTGGTGGACAGC 1230
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1171 GCCACGCAGCCTTTGAATGGGCCAGTGATTGAGGGCTCCTTCCCGTTGCTGGTGGACAGC 1230

Qy         1201 AGTCCTCGGGCTCTGAGCCAGTGCCAGCGTCCAGCCAGTGATTCCTGCCTGGCTGCTGGTGACATCTTA 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 AGTCCTCGGGCTCTGAGCCAGTGCCAGCGTCCAGCCAGTGATTCCTGCCTGGCTGCTGGTGACATCCTA 1260

Qy         1231 AGTCCTCGGGCTGCTGAGCCAGTGCCAGCGTCCAGCCAGTGAATTCCTGGCCTGGTGCTGTGACATCCTA 1290
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1231 AGTCCTCGGGCTGCTGAGCCAGTGCCAGCGTCCAGCCAGTGAATTCCTGGCCTGGTGCTGTGACATCCTA 1290

Qy         1261 GCCCTGGGTTTTTGGCCCTCCTTTTTGGCTGTCTCACGCAGGCCGTTCCTTGGCGAGATGAGA 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 GCCCTGGGTTTTTGGCCCTCCTTTTTGGCTGTCTCACGCAGGCCGTTCCTTGGCGAGATGAGA 1320

Qy         1291 GCCCTGGTTTTTGGCCTCCTTTTTGGCTGTCTCACGCAGGCCGTTCCTTGTGTCGAGATGAGA 1350
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1291 GCCCTGGTTTTTGGCCTCCTTTTTGGCTGTCTCACGCAGGCCGTTCCTTGTGTCGAGATGAGA 1350

Qy         1321 AGGCAGCACAGAGAGGGGGAACCAAAGGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTAGCCGAG 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 AGGCAGCACAGAGAGGGGGAACCAAAGGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTAGCCGAG 1380
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RESULT 11
ABX76124

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridies to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

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CC   hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC   bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC   for diagnostic purposes and as targets for screening for therapeutic
CC   compounds that modulate lung cancer, such as antibodies. Sequences
CC   ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC   invention
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 318 T; 0 U; 0 Other;

Query Match            100.0%;  Score 1522;  DB 8;  Length 1552;
Best Local Similarity  100.0%;
Matches  1522;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 ACAGTCAGCCGACCATGGCTCCCCTGTCCCCTCCCTCTGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTCAGCCGACCATGGCTCCCCTGTCCCCTCCCTCTGTTGATCCCGGCC 60

Qy     61 CCTGCTCCAGGCGCTCACTGTGCAACTGCTGCTTCCCTCTGTTGATCCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGCGCTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCCAT 150

Qy    121 CCCCAGAGAGGTTGCCCCGGATGCAGGAGAGATTCCCCCTTGGGGGAGGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCCAGAGAGGTTGCCCCGGATGCAGGAGAGATTCCCCCTTGGGGGAGGAA 180

Qy    181 GATGACCCACTGGGCGGAGGAGGATTCACCCAGAGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGGAGGAGGATTCACCCAGAGAGGAGGAT 270

Qy    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCCGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAATCAGAGAAGAGAGGCTCCCTGAAGTTAGAG 360
          ||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAATCAGAGAAGAGAGGCTCCCTGAAGTTAGAG 390

Qy    361 GAGGCTCCTGGAGAGTCCTGAAGAACCCCAGAATAAATGCCACAGGA 420
          |||||||||||||||||||||||||||||||||||||||||||
Db    391 GAGGCTCCTGGAGAGTCCTGAAGAACCCCAGAATAAATGCCACAGGA 450

Qy    421 GACCAGAGTCATTGGGCGCTATGGAGGCAGACCCGCCTGGGT 480
          |||||||||||||||||||||||||||||||||||||||
Db    451 GACCAGAGTCATTGGGCGCTATGGAGGCAGACCCGCCTGGGT 510

Qy    481 GCGGGCCGGCCTTCCCAGTCCCCGGTGGATATCCGCCCCCAGC 540
          ||||||||||||||||||||||||||||||||||||||||
Db    511 GCGGGCCGGCCTTCCCAGTCCCCGGTGGATATCCGCCCCCAGC 570

Qy    541 CTGCGCGCCCCTGGAACTCCTGGGCGCTTCCAGCTCCCAGA 600
          ||||||||||||||||||||||||||||||||||||||
Db    571 CTGCGCGCCCCTGGAACTCCTGGGCGCTTCCAGCTCCCAGA 630

Qy    601 AACAATGGCCACAGTGTCCAACTGACCCTGCCCTGCCC 660
          ||||||||||||||||||||||||||||||||||||
Db    631 AACAATGGCCACAGTGTCCAACTGACCCTGCCCTGCCC 690

Qy    661 GGGCGGCGGAGTACCCGGCGTCTGCACTCGGGCGCTGCAGG 720
          |||||||||||||||||||||||||||||||||||||
Db    691 GGGCGGCGGAGTACCCGGCGTCTGCACTCGGGCGCTGCAGG 750

Qy    721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCAC 780
          ||||||||||||||||||||||||||||||||||||||||||
Db    751 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCAC 810

Qy    781 ACCGGCCTTTGCCAGAGTTGACAGAGGCCTTGGGCGCGGCCC 840
          |||||||||||||||||||||||||||||||||||||||
Db    811 ACCGGCCTTTGCCAGAGTTGACAGAGGCCTTGGGCGCGGCCC 870

Qy    841 GCCTTTCTGGAGGAGGGCCCCGGAGGGGAGGAAGAAACAGTGCC 900
          ||||||||||||||||||||||||||||||||||||||||
Db    871 GCCTTTCTGGAGGAGGGCCCCGGAGGGGAGGAAGAAACAGTGCC 930

Qy    901 GAAGAAATGGCTGAGGAGAGGGCTCAGGAGACTCCCAGGACTGGA 960
          |||||||||||||||||||||||||||||||||||||||||
Db    931 GAAGAAATCGCTGAGGAGAGGGCTCAGGAGACTCCCAGGACTGGA 990

Qy    961 CTGCCCTCTGACTTCAGCCGCGCTACTTCACTTCCAATATGAGG 1020
          ||||||||||||||||||||||||||||||||||||||||
Db    991 CTGCCCTCTGACTTCAGCCGCGCTACTTCACTTCCAATATGAGG 1050

Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAGTG 1080
          |||||||||||||||||||||||||||||||||||||||
Db   1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAGTG 1110

Qy   1081 CACACCCTCTCTGACACCCTGTGGGGACCCTGGGACTCTCGG 1140
          ||||||||||||||||||||||||||||||||||||||
Db   1111 CACACCCTCTCTGACACCCTGTGGGGACCCTGGGACTCTCGG 1170

Qy   1141 GCGAGCGGCAGCCTTTGAAATGGGCGAGTGATTGAGGCCTCCTT 1200
          ||||||||||||||||||||||||||||||||||||||||
Db   1171 GCGAGCGGCAGCCTTTGAAATGGGCGAGTGATTGAGGCCTCCTT 1230

Qy   1201 AGTTCCTCGGGCGGCTGCTGAGCCCAGTCAATTCCTGCCGT 1260
          |||||||||||||||||||||||||||||||||||||
Db   1231 AGTTCCTCGGGCGGCTGCTGAGCCCAGTCAATTCCTGCCGT 1290

Qy   1261 GCCCTGGTTTTTGGCTCCTCCTTTTGCTGTCACCAGCGTGGCG 1320
          |||||||||||||||||||||||||||||||||||||||
Db   1291 GCCCTGGTTTTTGGCTCCTCCTTTTGCTGTCACCAGCGTGGCG 1350

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTGAGCTACCGCC 1380
          |||||||||||||||||||||||||||||||||||||||
Db   1351 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTGAGCTACCGCC 1410

Qy   1381 ACTGGAGCCTAGAGGCTGGATCTTCGAGAATGTGAGAAGCCAG 1440
          |||||||||||||||||||||||||||||||||||||||
Db   1411 ACTGGAGCCTAGAGGCTGGATCTTCGAGAATGTGAGAAGCCAG 1470

Qy   1441 GGAGCCGCGGTAAACTGTCCCGTCCCTCCATTATGCCCAGAAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||
Db   1471 GGAGCCGCGGTAAACTGTCCCGTCCCTCCATTATGCCCAGAAAATT 1530

Qy   1501 TTTTAAAAATAAATATTTATAAT 1522
          |||||||||||||||||||||
Db   1531 TTTTAAAAATAAATATTTATAAT 1552
```

RESULT 12
ADG89343

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ID   ADG89343 standard; DNA; 1552 BP.
XX
AC   ADG89343;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Cancer detection method related gene #6.
XX
KW   dsj cancer; gene expression;
KW   estrogen receptor-positive invasive breast cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003078662-A1.
XX
PD   25-SEP-2003.
XX
PF   12-MAR-2003; 2003WO-US007713.
XX
PR   13-MAR-2002; 2002US-0364890P.
PR   18-SEP-2002; 2002US-0412049P.
XX
PA   (GENO-) GENOMIC HEALTH INC.
XX
PI   Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX
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DR   WPI; 2003-767536/72.
XX
PT   Predicting clinical outcome for a patient diagnosed with cancer comprises
PT   determining the expression level of one or more genes, and compared to
PT   the amount found in a reference cancer tissue set.
XX
PS   Disclosure; SEQ ID NO 291; 198pp; English.
XX
CC   The invention relates to a method of predicting clinical outcome for a
CC   patient diagnosed with cancer by determining the expression level of one
CC   or more genes, or their expression products, selected from p53BP2,
CC   cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a cancer
CC   tissue obtained from the patient, normalized against control gene(s), and
CC   compared to the amount found in a reference cancer tissue set. The
CC   specification also discloses an array comprising polynucleotides
CC   hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEGP1, Ki-
CC   67, GSTM1, CA9, PR, BBC3, NME1, SURV, GATA3, TFRC, YB-1, DPYD, GSTM3,
CC   RPS6KB1, Src, Chk1, ID1, EstR1, p27, CCNB1, XIAP, Chk2, CDC25B, IGF1R,
CC   AK055699, PI3KC2A, TGFB3, BAGI1, CYP3A4, EpCAM, VEGFC, pS2, hENT1, WISP1,
CC   HNF3A, NFKBP65, BRCA2, EGFR, TK1, VDR, Contig51037, pENT1, EPHX1, IFIA,
CC   CDH1, HIF1t, IGFBP3, CTSB, Her2 and DIABLO, immobilized on a solid
CC   surface. The methods are useful for predicting clinical outcome for a
CC   patient diagnosed with cancer, classifying cancer, and predicting the
CC   likelihood of long-term survival of a breast cancer patient, or a patient
CC   diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC   positive invasive breast cancer. This sequence corresponds to a gene
CC   sequence whose expression is detected by the method of the invention.
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match   100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        1 ACAGTCAGCGCAATGGCTCCCCTGTGCCCCAGCCTCCCTCTGTTGATCCCGGCC          60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       31 ACAGTCAGCGCAATGGCTCCCCTGTGCCCCAGCCTCCCTCTGTTGATCCCGGCC          90

Qy       61 CCTGCTCCAGGGCCTCACGTGCAACTGCTGCGTTCTCATGGCTGTCCAT        120
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db       91 CCTGCTCCAGGGCCTCACGTGCAACTGCTGCGTTCTCATGGCTGTCCAT        150

Qy      121 CCCCGAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCGTTGGAGAGGCTCTTCTGGGGAA        180
Db      151 CCCCGAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCCGTTGGAGAGGCTCTTCTGGGGAA        210

Qy      181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAAGGGAATTCACCCAGAGGAGGGAT        240
Db      211 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAAGGGAATTCACCCAGAGGAGGGAT        270

Qy      241 CCACCCCGGAGGAGGATCTACCTGGAGGAGGATCTACCTACCTACCTGTT        300
Db      271 CCACCCCGGAGGAGGATCTACCTGGAGGAGGATCTACCTACCTACCTGTT        330

Qy      301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCGTGAAGTTAGAGGATCTACCT        360
Db      331 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCGTGAAGTTAGAGGATCTACCT        390

Qy      361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGGACAAAGAAGGGAT        420
Db      391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGAGGACAAAGAAGGGAT        450

Qy      421 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCCCGTGTCCCCAGCCTGC        480
Db      451 GACCAGAGTCATTGGGCGCTATGGAGGCGACCCCCGTGTCCCCAGCCTGC        510

Qy      481 GCGGGCGCCCCTGGAACTCCTGGGGTCGCGGCTCGCCCCGCGCGGCTTCGC        540
Db      511 GCGGGCGCCCCTGGAACTCCTGGGGTCGCGGCTCGCCCCGCGCGGCTTCGC        570

Qy      541 GACCAGAGTCAATTGGGCGTATGGAGGGCGACCCGGCTTCGCCCCGGC        600
Db      571 CTGCGCGCCCCTGGAACTCCTGGGGCTTCCAGCTCGCCCCGCGCGGC        630
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Qy      601 AACAAATGGCCACAGTGTGCAACTGACCCTTGCCTGCCTCCCTGGGGTAGAGTGGCTCTCGGGGTCC        660
Db      631 GGGCGGGGGAGTACCGGGCGTCTGCAGCTGCAACTGACCCTTGCCTGCCTCCCTGGGGTAGAGTGGCTCTCGGGGTCC        720

Qy      661 GGGGCGGGAGGAGTACCCGGGCTCTGCAGCTGCATCTCTGCAGGTCGTTCGGGTCGTTCCGGGC        720
Db      721 TCGGAGCACACTGTGGAAGGCCACCGGTTCCCTGCCGAGGATCCACTGGGGCGGGGCTGCAGGTCGTTCGGGTCGTTCCGGGC        780

Qy      721 TCGGAGCACACTGTGGAAGGCCACCGGTTCCCTGCCGAGGATCCACTGGGGCGGGGCTGCAGC        780
Db      751 TCGGAGCACACTGTGGAAGGCCACCGGTTCCCTGCCGAGGATCCACTGGGGCGGGGCTGCAGC        810

Qy      781 ACCCGCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCCGCGGGAGGCCCTGCGGTCGTTGGGCC        840
Db      811 ACCCGCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCCGCGGGAGGCCCTGCGGTCGTTGGGCC        870

Qy      841 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCTTATGGAGCAGTTGCTTGTCTCGCTTG        900
Db      871 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCTTATGGAGCAGTTGCTTGTCTCGCTTG        930

Qy      901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGAGGACTGGACAGTATATCTGCACTC        960
Db      931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGAGGACTGGACAGTATATCTGCACTC        990

Qy      961 CTGCCCTCTGACTTCAGCCGCCTACTTCCAAATATGAGGGGGTCTCTGACTACACCCCCCGT        1020
Db      991 CTGCCCCTCTGACTTCAGCCGCCTACTTCCAAATATGAGGGGGTCTCTGACTACACCCCCCTGT        1050

Qy     1021 GCCCAGGCGGTGCATCTGGACTGTGTTTAACCAGACAGTGAATGCTGAGGTGGCTAAGCAGTC        1080
Db     1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGAATGCTGAGGTGGCTAAGCAGTC        1110

Qy     1081 CACACCCTTCTTCGACACCCTGTGGGAGGACCTGGTGACTCTCGGCGGCTAACAGCTGAACTTCCGA        1140
Db     1111 CACACCCTTCTTCGACACCCTGTGGGAGGACCTGGTGACTCTCGGCGGCTAACAGCTGAACTTCCGA        1170

Qy     1141 GCGACGCGAGCCCTTTGAACTGGGCGGAGTGATTGGAGGCGCCTCCTTCTCCTGCTGGTGGACAGC        1200
Db     1171 GGGACGCGAGCCCTTTGAACTGGGCGGAGTGATTGGAGGCGCCTCCTTCTCCTGCTGGTGGACAGC        1230

Qy     1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGTCCAGCTGAATTCCTGCCTGCTGGTGCACATCCTA        1260
Db     1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGTCCAGCTGAATTCCTGCCTGCTGGTGCACATCCTA        1290

Qy     1261 GCCCTGGTTTTTGGCCTTCCTTTTTCGTGTCACCAGCGGCTGCGCGTGCGCGTTCCTTGTGGTGCAGATGAGA        1320
Db     1291 GCCCTGGTTTTTGGCCTTCCTTTTTCGTGTCACCAGCGGCTGCGCGTGCGCGTTCCTTGTGGTGCAGATGAGA        1350

Qy     1321 AGGCAGCACAGAAGGGGGAACCAAAAGGGGGTGTGAGCTGAGCGTACCGCGGCAGAGAGGTAGCCCGAG        1380
Db     1351 AGGCAGCACAGAAGGGGGAACCAAAAGGGGGTGTGAGCTGAGCGTACCGCGGCAGAGAGGTAGCCCGAG        1410

Qy     1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG        1440
Db     1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG        1470

Qy     1441 GGAGCCGGTAACTGTCCTGCTCATTAGCCACTTCCTTTTAACTGCCAAGAAATT        1500
Db     1471 GGAGCCGGTAACTGTCCTGCTCATTAGCCACTTCCTTTTAACTGCCAAGAAATT        1530

Qy     1501 TTTTAAAATAAATATTTTATAAT        1522
Db     1531 TTTTAAAATAAATATTTTATAAT        1552
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DE   Human cancer related protein encoding cDNA SEQ ID NO:69.
XX
KW   Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW   heart disease; atherosclerosis; endometriosis; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO20030025138-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-US029560.
XX
PR   17-SEP-2001; 2001US-0323469P.
PR   20-SEP-2001; 2001US-0323887P.
PR   13-NOV-2001; 2001US-0350666P.
PR   08-FEB-2002; 2002US-0355145P.
PR   08-FEB-2002; 2002US-0355257P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI   Zlotnik A;
XX
DR   WPI; 2003-354600/33.
DR   P-PSDB; ABR58595.
XX
PT   New genes that are up-regulated or down-regulated in cancers, useful as
PT   markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT   therapeutic targets for screening drugs for treating these diseases.
XX
PS   Claim 8; Page 662; 767pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   comprises the sequence of any of the genes that are up-regulated or down-
CC   regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC   acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC   related gene nucleotide sequences which encode the proteins given in
CC   ABR58521 to ABR58709. Also described: (1) determining the presence or
CC   absence of a pathological cell in a patient; (2) an expression vector
CC   comprising a nucleic acid molecule described above; (3) a host cell
CC   comprising the vector; (4) an isolated polypeptide, which is encoded by
CC   the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC   of (4); (6) specifically targeting a compound to a pathological cell in a
CC   patient by administering to the patient the antibody above; and (7) a
CC   drug screening assay. The nucleic acid is useful as diagnostic markers or
CC   therapeutic targets. In particular, the nucleic acid is useful for
CC   diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC   bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC   pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC   atherosclerosis and endometriosis. The nucleic acid is also useful in
CC   drug screening, particularly for identifying agents for treating these
CC   pathologies
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1522;  DB 10;  Length 1552;
Best Local Similarity   100.0%;
Matches  1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 ACAGTCAGCCGCAATGGCTCCCCTGTGCCCAGCCCCTGGCTCCCTTCTGTTGATCCCGGCC 60
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Db     31 ACAGTCAGCCGCAATGGCTCCCCTGTGCCCAGCCCCTGGCTCCCTTCTGTTGATCCCGGCC 90

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGTGCTGTCACTGCTCCTTCTCTGTTGATGCCTGTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGCCTCACTGTGCAACTGTGCTGTCACTGCTCCTTCTCTGTTGATGCCTGTCCAT 150

Qy    121 CCCCAGAGAGGTTGCCCGGATGCAGGAGGATTCCCCGTTGGGAGGAGGAGGCTCTTCTGGGGAA 180
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Db    151 CCCCAGAGAGGTTGCCCGGATGCAGGAGGATTCCCCGTTGGGAGGAGGAGGCTCTTCTGGGGAA 210

Qy    181 GATGACCCACTGGGCGGAGGAGGATTGCCCAGTGAAGTGGATTCACCCAGAGAGGAGGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGGAGGAGGATTGCCCAGTGAAGTGGATTCACCCAGAGAGGAGGAT 270

Qy    241 CCACCCGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGAT 300
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Db    271 CCACCCGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGAT 330

Qy    301 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAATCAGAAGAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy    361 GAGGGCTTCCTTGGAGGATCCTCAAGGAACCCCAGAATAATGCCCAGGGAGCACAGGGGGAT 420
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Db    391 GAGGGCTTCCTTGGAGGATCCTCAAGGAACCCCAGAATAATGCCCAGGGAGCACAGGGGGAT 450

Qy    421 GACCAGAGTCATTGGCGCTATGGAGGGGACCCGCGGCCCCGGGGGTGTCCCCAGCCTGC 480
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Db    451 GACCAGAGTCATTGGCGCTATGGAGGGGACCCGCGGCCCCGGGGGTGTCCCCAGCCTGC 510

Qy    481 GCGGCGGCCGCTTCCAGTGCCCCGGTTGGGATGATCGCCCGCGCGGGGGCCCTTTCTGCGGCC 540
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Db    511 GCGGCGGCCGCTTCCAGTGCCCCGGTTGGGATGATCGCCCGCGCGGGGGCCCTTTCTGCGGCC 570

Qy    541 CTGCGCCCCCCTGGAACTCCTTGGGCTTCCCAGCTCTCCCGGGTGATATCCGGGCCCTTGC 600
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Db    571 CTGCGCCCCCCTGGAACTCCTTGGGCTTCCCAGCTCTCCCGGGTGATATCCGGGCCCTTGC 630

Qy    601 AACAAATGGGCCACAGTGTGCAAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 AACAAATGGGCCACAGTGTGCAAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGCC 690

Qy    661 GGGGCGGGGGAGTTACCCGGGGCTTGCACTGCCATCTGCACTGCACTGCCGTGTTCGTTGGGC 720
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Db    691 GGGGCGGGGGAGTTACCCGGGGCTTGCACTGCCATCTGCACTGCACTGCCGTGTTCGTTGGGC 750

Qy    721 TCGGGAGCACACTGTGGGAAGGCCACCGGTTTCCCGGGAGATCCACGTTGGTTCACCTCAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCGGGAGCACACTGTGGGAAGGCCACCGGTTTCCCGGGAGATCCACGTTGGTTCACCTCAGC 810

Qy    781 ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCCGCGGCCGGCCTGGGCGTGTTGGGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ACCGGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCCGCGGCCGGCCTGGGCGTGTTGGGC 870

Qy    841 GCCTTTCTCGGAGGAGGAGGAAAACAGTGGCCTATGAGCAGTTGCTGGTCGTGTCGCGTTG 900
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Db    871 GCCTTTCTCGGAGGAGGAGGAAAACAGTGGCCTATGAGCAGTTGCTGGTCGTGTCGCGTTG 930

Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGTCCCAGGACTGGACATATCTGCACTC 960
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Db    931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGTCCCAGGACTGGACATATCTGCACTC 990

Qy    961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTTCTCTGACTACACCGCCCTGT 1020
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Db    991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTTCTCTGACTACACCGCCCTGT 1050

Qy   1021 GCCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAACAGCAGTGAATGCTTAAGCAGCTC 1080
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Db   1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAACAGCAGTGATGCTTAAGCAGCTC 1110

Qy   1081 CACACCCTTCTGACACCCTGTGGGGACTGGGTGACTGGGTGACTGGGTGAACTTCGGA 1140
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Db   1111 CACACCCTTCTGACACCCTGTGGGGACTGGGTGACTGGGTGACTGGGTGAACTTCGGA 1170

Qy   1141 GCGACGGCAGCCTTTGAATGGGCGAGTGATTGAGGGCCTCCTTCCCCTGCTGGACAGC 1200
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Db   1171 GCGAGGCAGCCTTTGAATGGGCGAGTGATTGAGGGCCTCCTTCCCCTGCTGGACAGC 1230

Qy   1201 AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCTGCTGGTGACATCCTA 1260
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Db   1231 AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCCTGGCTGCTGGTGACATCCTA 1290
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Qy    1261  GCCCTGGTTTTGGCCTCCTTTTTGCTGTGTCACCAGCGTGCCGTTCGG 1320
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Db    1291  GCCCTGGTTTTGGCCTCCTTTTTGCTGTGTCACCAGCGTGCCGTTCGG 1350

Qy    1321  AGGGCACAGAGGGGGACCAAAAGGGGGTGTGAGCTACCGCGGGTAGCCCGAG 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1351  AGGGCACAGAGGGGGACCAAAAGGGGGTGTGAGCTACCGCGGGTAGCCCGAG 1410

Qy    1381  ACTGGAGCCTAGAGACGCTGGATTCTTGGAGAATGTCAGAAGCCAGACCATCTGAGGG 1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411  ACTGGAGCCTAGAGACGCTGGATTCTTGGAGAATGTCAGAAGCCAGACCATCTGAGGG 1470

Qy    1441  GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Db    1471  GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530

Qy    1501  TTTTAAAATAAATATTTATAAT 1522
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Db    1531  TTTTAAAATAAATATTTATAAT 1552
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Qy     1  ACAGTCAGCGCCATGGCTCCCCTGTGCCCCAGCCCTTGGCTCCCCTCGTTGATCCGGGCC 60
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Db    31  ACAGTCAGCGCCATGGCTCCCCTGTGCCCCAGCCCTTGGCTCCCCTCGTTGATCCGGGCC 90

Qy    61  CCTGCTCCAGGCCTCACTGTGCTGCTCCCCAGCCCTGCTGCTCCTTCTGATGCCTTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    91  CCTGCTCCAGGCCTCACTGTGCTGCTCCCCAGCCCTGCTGCTCCTTCTGATGCCTTCCAT 150

Qy   121  CCCCAGAGAGGTTGCCCCGGCAGGAGGAGGCTCTTCTGGGAGGAA 180
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Db   151  CCCCAGAGAGGTTGCCCCGGCAGGAGGAGGCTCTTCTGGGAGGAA 210

Qy   181  GATGACCCACTGGGCGGCGAGGAGGATCTGCCCAGTGAAGAAGGATTCACCCAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   211  GATGACCCACTGGGCGGCGAGGAGGATCTGCCCAGTGAAGAAGGATTCACCCAGAGGAGGAT 270

Qy   241  CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||
Db   271  CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGATCTACCT 330

Qy   301  GAAGTTAAGCCTAAATCAGAGAAGAGAGGGCTCCCTGAAGTTAGAGGACTTACTTACTGTT 360
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Db   331  GAAGTTAAGCCTAAATCAGAGAAGAGAGGGCTCCCTGAAGTTAGAGGACTTACTTACTGTT 390

Qy   361  GAGGGCTCCTGGGAGAATCCTCAAGAACCCCAGAATAAATGCCCACAGGGGACAAAGAAGG 420
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Db   391  GAGGGCTCCTGGGAGAATCCTCAAGAACCCCAGAATAAATGCCCACAGGGGACAAAGAAGG 450

Qy   421  GACCAGAGTCATTGGGCGCTATGGAGGGCGACCCGGCCCTGGCCCTGGGGTGTCCCCAGCCTGC 480
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Db   451  GACCAGAGTCATTGGGCGCTATGGAGGGCGACCCGGCCCTGGCCCTGGGGTGTCCCCAGCCTGC 510

Qy   481  GCGGGGCCGCCTTCCAGTTCCCCGGTGGATATCCGCCCGCCCCCCAGCGCTGCCCGGCCTTCTGCCGCGC 540
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Db   511  GCGGGGCCGCCTTCCAGTTCCCCGGTGGATATCCGCCCGCCCCCCAGCGCTGCCCGGCCTTCTGCCGCGC 570

Qy   541  CTGCGCGCCCCCTGGAACTCCTGGGCCTTCCAGTCCCCAGAAACTGCGCTCGGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   571  CTGCGCGCCCCCTGGAACTCCTGGGCCTTCCAGTCCCCAGAAACTGCGCTCGGC 630

Qy   601  AACAATGGCCACAGTGTTGCAACTGACCCTGCCTCTCCTCCGGCGGGGGGTCCC 660
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Db   631  AACAATGGCCACAGTGTTGCAACTGACCCTGCCTCTCCTCCGGCGGGGGGTCCC 660

Qy   661  GGGCGGGGAGTACGGGGCGTTCTGCAGCTCCATCTGCACTGGCGGCGTCGAGGTCGTTCCGGGC 720
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Db   691  GGGCGGGGAGTACGGGGCGTTCTGCAGCTCCATCTGCACTGGCGGCGTCGAGGTCGTTCCGGGC 750

Qy   721  TCGGAGCACACTGTGGAAGGGCACCGTTCCCTGCCAGATCCAGCGGTCACCTCAGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751  TCGGAGCACACTGTGGAAGGGCACCGTTCCCTGCCAGATCCAGCGGTCACCTCAGC 810

Qy   781  ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCCTGGGCCGTGGGCCTGTGGTTGGCC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811  ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGGCCTGGGCCGTGGGCCTGTGGTTGGCC 870

Qy   841  GCCTTTCTGGAGGAGGGCCCCGGAAGAGAAAACAGTGCCTATGAGCCAGTGCGTCACTTCCGGCTTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871  GCCTTTCTGGAGGAGGGCCCCGGAAGAGAAAACAGTGCCTATGAGCCAGTGCGTCACTTCCGGCTTG 930

Qy   901  GAAGAAATCGCTGAGGAGAAGGCTCAGGACACTCAGGTCCAGACGACTCAGGTCACATATGTCGACTC 960
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Db    931  GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC  990

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Db    991  CTGCCCCTTGACTTCAGCCGCTACTTCCAATATGAAGGGGTCTCTGACTACACCGCCCTGT 1050

Qy   1021  GCCCAGGGGTGTCATCTGGACTGTGTTTTAACCAGACAGCAGTGATGTCGAGTCGAAGCAGTC 1080
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Db   1051  GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGCAGTGATGTCGAGTCGAAGCAGTC 1110

Qy   1081  CACACCCTTCTCTGACACCCTGTGGGGGACCTGGTGGACTACAGCTGAACTTCCGA 1140
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Db   1111  CACACCCTTCTCTGACACCCTGTGGGGGACCTGGTGGACTACAGCTGAACTTCCGA 1170

Qy   1141  GCGACGCAGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGACAGC 1200
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Db   1171  GCGACGCAGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGACAGC 1230

Qy   1201  AGTCCTCCGGGCTCGTGAGCCAGTCCAGCTGAGTGCCTGCTGGTGCACATCCTA 1260
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Db   1231  AGTCCTCCGGGCTCGTGAGCCAGTCCAGCTGAGTGCCTGCTGGTGCACATCCTA 1290

Qy   1261  GCCCTGGTTTTGGCCTCCCTTTTGGCTGTCACCAGGCGTGCGGTTCCTTGTGCAGATGAGA 1320
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Db   1291  GCCCTGGTTTTGGCCTCCCTTTTGGCTGTCACCAGGCGTGCGGTTCCTTGTGCAGATGAGA 1350

Qy   1321  AGGCAGCACAGGAAGGGGGAACCAAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
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Db   1351  AGGCAGCACAGGAAGGGGGAACCAAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1410

Qy   1381  ACTGGAGCCTAGAGGCTGGATCTTCTTGGAGAATGTGAGGAGGCCAGCAGAGGGCCATCTCTGAGGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411  ACTGGAGCCTAGAGGCTGGATCTTCTTGGAGAATGTGAGGAGGCCAGCAGAGGGCCATCTCTGAGGG 1470

Qy   1441  GGAGCCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471  GGAGCCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT 1530

Qy   1501  TTTTAAAATAAATATTTATAAT 1522
           ||||||||||||||||||||||
Db   1531  TTTTAAAATAAATATTTATAAT 1552
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RESULT 15

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ID   ADN39704 standard; cDNA; 1552 BP.
XX
AC   ADN39704;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C76.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularisation syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200304266l-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0343393P.
PR   03-DEC-2001; 2001US-0335394P.
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PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0395839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-486649/44.
DR   P-PSDB; ADN39921.
XX
PT   Claim 8; SEQ ID NO C76; 1385pp; English.
XX
PS   Claim 8; SEQ ID NO C76; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune disease, retinal
CC   neovascularisation syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
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Query Match          100.0%;  Score 1522;  DB 11;  Length 1552;
Best Local Similarity  100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy     1  ACAGTCAGCCGCATGGCTCCCCTGTGCCCAGCCCCTGGCTCCCTCTGTTGATCCGGCC  60
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Db    31  ACAGTCAGCCGCATGGCTCCCCTGTGCCCAGCCCCTGGCTCCCTCTGTTGATCCGGCC  90

Qy    61  CCTGCTCCAGGCCTCACTGTCGAACTGCTGCTGTCACTGCTTCTGATGCCGTGTCCAT 120
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Db    91  CCTGCTCCAGGCCTCACTGTCGAACTGCTGCTGTCACTGCTTCTGATGCCGTGTCCAT 150

Qy   121  CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTGGGAGGAGGCTCTTCTGGGGAA 180
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Db   151  CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTGGGAGGAGGCTCTTCTGGGGAA 210

Qy   181  GATGACCCACTGGGCGGAGGAGGATTCGCCCAGTGAAGAGGAGATTCACCCAGAGGAGGAT 240
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Db   211  GATGACCCACTGGGCGGAGGAGGATTCGCCCAGTGAAGAGGAGATTCACCCAGAGGAGGAT 270

Qy   241  CCACCCGGAGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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Db   271  CCACCCGGAGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
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Qy   301 GAAGTTAAGCCTAAATCAGAGAAGAAGAGGGCTCCCTGAAGTAGGTTAGAGGAICTACCTACTGTT 360
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Db   331 GAAGTTAAGCCTAAATCAGAGAAGAAGAGGGCTCCCTGAAGTTAGAGGAICTACCTACTGTT 390

Qy   361 GAGGCTCCTGGAGAICCTCAAGAACCCAGAAATAAATGCCCACAGGGACAAAGAAGGGGAT 420
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Db   391 GAGGCTCCTGGAGAICCTCAAGAACCCAGAAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy   421 GACCAGAGAGTCAITGGCGCTIATGGAGGCGACCCCGCCCCGGGGTGTCCCCCAGCCCTGC 480
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Db   451 GACCAGAGTCAITGGCGCTIATGGAGGCGACCCCGCCCCGGGGTGTCCCCCAGCCCTGC 510

Qy   481 GCGGGGCGGCTTCCAGTCCCGGTGGATAICGGCCCCCCAGCTCGGGCGGCCTTCTGCCCGGCC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   511 GCGGGGCCGCTTCCAGTCCCGGTGGATAICCGGCCGCGGCCTTCTGCCCGGCC 570

Qy   541 CTGGGCCCCCTGGAACTCCTGGGGCTTCAGCTCCCGCGCCTCCCAGAACTGGGCCCTGCCC 600
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Db   571 CTGGGCCCCCTGGAACTCCTGGGGCTTCAGCTCCCGCGCCTCCCAGAACTGGGCCCTGCCC 630

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Qy   721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGAICCAGTGGTCACCTCAGC 780
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Qy  1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGACCAGAGGGCAICTGAGGG 1440
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Search completed: February 6, 2005, 04:08:57
Job time : 735 secs

OM nucleic - nucleic search, using sw model

           GenCore version 5.1.6
           Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 6, 2005, 03:50:49 ; Search time 154 Seconds
                               (without alignments)
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Title: US-09-967-237A-1
Perfect score: 1522
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Scoring table: IDENTITY_NUC
Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Maximum DB seq length: 2000000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries

Database :   Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1522	100.0	1522	2	US-08-481-658B-1	Sequence 1, Appli
2	1522	100.0	1522	2	US-08-477-504A-1	Sequence 1, Appli
3	1522	100.0	1522	2	US-08-486-756A-1	Sequence 1, Appli
4	1522	100.0	1522	2	US-08-485-862B-1	Sequence 1, Appli
5	1522	100.0	1522	3	US-08-787-739-1	Sequence 1, Appli
6	1522	100.0	1522	3	US-08-487-077A-1	Sequence 1, Appli
7	1522	100.0	1522	2	US-08-485-863A-1	Sequence 1, Appli
8	1522	100.0	1522	3	US-08-485-049D-1	Sequence 1, Appli
9	1522	100.0	1522	3	US-09-178-115-1	Sequence 1, Appli
10	1522	100.0	1522	4	US-09-772-719B-1	Sequence 1, Appli
11	1522	100.0	1522	4	US-08-477-504A-1	Sequence 1, Appli
12	1522	100.0	1522	4	US-08-260-190-5	Sequence 23, Appl
13	1416.8	93.1	5052	4	US-08-260-190-23	Sequence 5, Appl
14	1399	91.9	1399	4	US-08-335-469-1	Sequence 1, Appli
15	1399	91.9	1399	5	US-07-964-589-1	Sequence 1, Appli
16	1302.8	85.6	1397	5	PCT-US93-02024-1	Sequence 1, Appli
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18	414.4	27.2	10898	2	US-08-477-504A-5	Sequence 5, Appli
19	414.4	27.2	10898	2	US-08-486-756A-5	Sequence 5, Appli
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21	414.4	27.2	10898	3	US-08-487-077A-5	Sequence 5, Appli
22	414.4	27.2	10898	2	US-08-485-862B-5	Sequence 5, Appli
23	414.4	27.2	10898	3	US-08-487-739-5	Sequence 5, Appli
24	414.4	27.2	10898	3	US-08-485-049D-5	Sequence 5, Appli
25	414.4	27.2	10898	3	US-09-178-115-5	Sequence 5, Appli
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27	414.4	27.2	10898	3	US-09-177-776-5	Sequence 5, Appli
28	414.4	27.2	10898	4	US-09-772-719B-5	Sequence 5, Appli
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33	413.4	27.2	415	3	US-08-487-077A-28	Sequence 28, Appl
34	413.4	27.2	415	2	US-08-485-863A-28	Sequence 28, Appl
35	413.4	27.2	415	3	US-08-485-049D-28	Sequence 28, Appl
36	413.4	27.2	415	3	US-08-787-739-28	Sequence 28, Appl
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43	233.4	15.3	470	2	US-08-485-862B-55	Sequence 5, Appl
44	233.4	15.3	470	3	US-08-787-739-55	Sequence 5, Appl
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ALIGNMENTS

RESULT 1
US-08-481-658B-1

Sequence 1, Application US/08481658B
Patent No. 5955075

; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-481-658B-1

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Matches 1522;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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; Sequence 1, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
;   APPLICANT: Zavada, Jan
;   APPLICANT: Pastorekova, Silvia
;   APPLICANT: Pastorek, Jaromir
;   TITLE OF INVENTION: MN Gene and Protein
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Leona L. Lauder
;   STREET: 6 Mariposa Court
;   CITY: Tiburon
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94920
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/477,504A
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/260,190
;   FILING DATE: 15-JUN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lauder, Leona L.
;   REGISTRATION NUMBER: 30,863
;   REFERENCE/DOCKET NUMBER: D-0021.3D
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-435-2034
;   TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1522 base pairs
;   TYPE: nucleic acid

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;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
US-08-477-504A-1

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Best Local Similarity  100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy  361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAAGGGGAT 420
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Db  361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAAGAAGGGGAT 420

Qy  421 GACCAGAGTCATTGGGCGTATGGAGGGCGACCCCGCCCCGGGGTGTCCCCAGCCCTGC 480
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Db  421 GACCAGAGTCATTGGGCGTATGGAGGGCGACCCCGCCCCGGGGTGTCCCCAGCCCTGC 480

Qy  481 GCGGGGCCGCTTCCAGTCCCCGGTGGATATCCGGACTCGCCGCCTTCTGCCCGGCC 540
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Db  481 GCGGGGCCGCTTCCAGTCCCCGGTGGATATCCGGACTCGCCGCCTTCTGCCCGGCC 540

Qy  541 CTGCGCCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCCGCCTCCCAGAACTGCGCGCTGCCC 600
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Db  541 CTGCGCCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCCGCCTCCCAGAACTGCGCGCTGCCC 600

Qy  601 AACAATGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTCAGGTGGGTCCC 660
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Db  601 AACAATGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTCAGGTGGGTCCC 660

Qy  661 GGGGCGGGAGTACCGGGCTCTGCAGCTGCATCGCGAGCTGCCAGGTCGGTCCCGGGC 720
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Db  661 GGGGCGGGAGTACCGGGCTCTGCAGCTGCATCGCGAGCTGCCAGGTCGGTCCCGGGC 720

Qy  721 TCCGAGCACACTGTGGAAGGGCCACCGGTTTCCCCTGCGAGATCCAACTGGGGTTCACCTCAGC 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TCCGAGCACACTGTGGAAGGGCCACCGGTTTCCCCTGCGAGATCCAACTGGGGTTCACCTCAGC 780

Qy  781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCGCCCTGGCCGGGCCGCCTGGCC 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCGCCCTGGCCGGGCCGCCTGGCC 840

Qy  841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGAGAGTTGCTGTTCGCTTG 900
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Db  841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGAGAGTTGCTGTTCGCTTG 900

Qy  901 GAAGAAATCGCTGAGGAAGGGCTCAGGAGACTCAGGTCCCAGGACTAGGTCCCAGGACATATCTGCACTC 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GAAGAAATCGCTGAGGAAGGGCTCAGGAGACTCAGGTCCCAGGACTAGGTCCCAGGACATATCTGCACTC 960

Qy  961 CTGCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTTCTCTGACTACACCGGCCCCTGT 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 CTGCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTTCTCTGACTACACCGGCCCCTGT 1020

Qy 1021 GCCCAGGGGTGTCATCTGGGACTGTGTTTAACCAGAGACAGTGATGATGCCAGAGGCTC 1080
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Db 1021 GCCCAGGGGTGTCATCTGGGACTGTGTTTAACCAGAGACAGTGATGATGCCAGAGGCTC 1080

Qy 1081 CACACCCTCTCTGACACCCCTGGGGGACCTGGGTGACTCTGGGGCTRCACAGCTGAACTTCCGA 1140
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Db 1081 CACACCCTCTCTGACACCCCTGGGGGACCTGGGTGACTCTGGGGCTRCACAGCTGAACTTCCGA 1140

Qy 1141 GCGACGGCAGCCCTTTGAAATGGGCGAGTGATTGAGGGCTCCTTCCCCTGCCTGCTGGAGGACAGC 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GCGACGGCAGCCCTTTGAAATGGGCGAGTGATTGAGGGCTCCTTCCCCTGCCTGCTGGAGGACAGC 1200

Qy 1201 AGTCCTTCGGGGCTGCTGAGCCAGCCCAGCTCAGGTTCCTGCTGGTTGCTGGTGACATCCTA 1260
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Db 1201 AGTCCTTCGGGGCTGCTGAGCCAGCCCAGCTCAGGTTCCTGCTGGTTGCTGGTGACATCCTA 1260

Qy 1261 GCCCTTGGGGTTTTTGGGCCTCCCTTTTTGGTTGTGTCACCACGCGTCGGGGTTCCTTGTGCAGATGAGA 1320
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Db 1261 GCCCTTGGGGTTTTTGGGCCTCCCTTTTTGGTTGTGTCACCACGCGTCGGGGTTCCTTGTGCAGATGAGA 1320

Qy 1321 AGGCAGCACAGAAGGGGGAACCAAAGGGGGGTGTGAGCTACCGCCCCCAGCGACAGAGGTAGCCGAG 1380
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Db 1321 AGGCAGCACAGAAGGGGGAACCAAAGGGGGGTGTGAGCTACCGCCCCCAGCGACAGAGGTAGCCGAG 1380

Qy 1381 ACTGGAGCCTAGAGGGCTGGATCTTGGGAGAATGTGAGAAGCCAGCGACGAGGCCATCTGAGGG 1440
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Db 1381 ACTGGAGCCTAGAGGGCTGGATCTTGGGAGAATGTGAGAAGCCAGCGACGAGGCCATCTGAGGG 1440

Qy 1441 GGAGCGCGGTAACTGTCCCGTCCGCTCATTAATGCCACTTCCTTTTAACTGCCAAGAAAATT 1500
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Db 1441 GGAGCGCGGTAACTGTCCCGTCCGCTCATTAATGCCACTTCCTTTTAACTGCCAAGAAAATT 1500

Qy 1501 TTTTAAAATAAATATTTTATAAT 1522
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Db 1501 TTTTAAAATAAATATTTTATAAT 1522
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RESULT 3
US-08-486-756A-1
; Sequence 1, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
;   APPLICANT: Zavada, Jan
;   APPLICANT: Pastorekova, Silvia
;   APPLICANT: Pastorek, Jaromir
;   TITLE OF INVENTION: MN Gene and Protein
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Leona L. Lauder
;   STREET: 6 Mariposa Court
;   CITY: Tiburon
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94920
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/486,756A
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/260,190
;   FILING DATE: 15-JUN-1994
;   ATTORNEY/AGENT INFORMATION:

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;   NAME: Lauder, Leona L.
;   REGISTRATION NUMBER: 30,863
;   REFERENCE/DOCKET NUMBER: D-0021.3C
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-435-0727
;     TELEFAX: 415-435-2034
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1522 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;   US-08-486-756A-1
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Query Match           100.0%;  Score 1522;  DB 2;  Length 1522;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy     1 ACAGTCAGCGCAATGGCTCCCCTGTGTGCCCCCAGCCCACGCCCCTGGCCTCCCCTCGCCC    60
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Qy    61 CCTGCTCCAGGCCTCACTGTCGCAACTGCTGCTGCTTCTGATGCCTGTCCAT           120
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Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTCTTCTGGGGAA   180
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Db   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTCTTCTGGGGAA  180

Qy   181 GATGACCCCACTGGGCGAGGAGATCTCCCCAGTGTAAGAGGAGGATTCACCCAGAGGAGGAT  240
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Qy   301 GAAGTTAAGCCTAAATCAGAAGAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT   360
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Qy   361 GAGGCTCCTGGAGATCCTCAAGAAACCCCAGAATAATGCCCACAGGGACAAAGAGAGGGAT   420
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Db   361 GAGGCTCCTGGAGATCCTCAAGAAACCCCAGAATAATGCCCACAGGGACAAAGAGAGGGAT  420

Qy   421 GACCAGAGTCATTGGGCCGCTATGGGAGGGGGACCCGCGCCCTGGGCGTGTCCCCAGCCTGC   480
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Db   421 GACCAGAGTCATTGGGCCGCTATGGGAGGGGGACCCGCGCCCTGGGCGTGTCCCCAGCCTGC  480

Qy   481 GCGGGGCCGCTTCCAGTCCCCGGGTGGGATATCCGGCCCCGGCCCTTCTGCCCCGGGCC     540
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Qy   541 CTGCGCCCCCTGGAACTCCTGGGCCTTCCAGCTCCCGCTCCCAGAACTGCGCCTGCGC     600
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Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTCCTGGGCGTTGGGGTCCC     660
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Qy   661 GGGCCGGGAGTACCGGGCTCGCAGCTGCAACTGGCCTGGAGGTCGTCCGGGC      720
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Db   661 GGGCCGGGAGTACCGGGCTCGCAGCTGCAACTGGCCTGGAGGTCGTCCGGGC     720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC    780
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Qy   781 ACCGGCCTTTGCCCAGGAGTTGACGAGGCCGTTGGGGCGGGGCCCGGCCCTGGGCGTGTTGGGCC   840
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Qy   841 GCCTTTCTTCTGGAGGAGGAGGGCCCGGGCGGAGGAAAACAGTGCCCTATGAGACAGTTGCCTG    900
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Qy   901 GAACAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACATGGGACATATCTCCACTC    960
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Qy   961 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACCGCCCTGT   1020
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Db  1021 GCCCAGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATGCTGAGGTGCTAAGCAGCTC  1080

Qy  1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCGCGGCTACACGTGAACTTCCGA   1140
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Db  1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCGCGGCTACACGTGAACTTCCGA  1140

Qy  1141 GCGAGCAGCGCCTTTGAATGGGCGGAGTGAATTGAGGGCCTCCTTCCCTGCCTGGGAGTGGGACAGC   1200
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Qy  1201 AGTCCTCGGGCGTGCTGACCCAGTCCAGTGAATTCCGTCCCTGGCCTGCCTTCCGCTGGGAGCATCCTA   1260
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Db  1201 AGTCCTCGGGCGTGCTGACCCAGTCCAGTGAATTCCGTCCCTGGCCTGCCTTCCGCTGGGAGCATCCTA  1260

Qy  1261 GCCCTGGTTTTGGGCCTCCTTTTTTGTGTCACCCAGCGTCGCGTCCTGTCTGCAGATGAGA   1320
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Qy  1381 ACTGGAGGCCTAGAGGCTGGATCTTGGAGGAAAGTGAGAAGCCAGCCAGAGGGCATCTGAGGG   1440
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Qy  1441 GGAGCCGGTAACTGTCCTGTCCCACTCCACTTCCTTTTTTTAACTGCCAAGAAATT    1500
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Qy  1501 TTTTAAAATAAAATATTTATAAT   1522
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Db  1501 TTTTAAAATAAAATATTTATAAT  1522
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RESULT 4
US-08-485-862B-1
Sequence 1, Application US/08485862B
Patent No. 5989838
GENERAL INFORMATION:
;   APPLICANT: Zavada, Jan
;   APPLICANT: Pastorekova, Silvia
;   APPLICANT: Pastorek, Jaromir
;   TITLE OF INVENTION: MN Gene and Protein
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Leona L. Lauder
;     STREET: 6 Mariposa Court
;     CITY: Tiburon
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94920
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  Patentin Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,862B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,504
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;   ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3D
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;   INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH:  1522 base pairs
;         TYPE:  nucleic acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
;      HYPOTHETICAL:  NO
;      ANTI-SENSE:  NO
US-08-485-862B-1

Query Match             100.0%;  Score 1522;  DB 2;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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(Sequence alignment lines — Query (Qy) and Database (Db) rows numbered in increments of 60, from positions 1 through 1522)

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;  TITLE OF INVENTION: MN Gene and Protein
;  NUMBER OF SEQUENCES: 96
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Leona L. Lauder
;  STREET: 369 Pine Street, Suite 610
;  CITY: San Francisco
;  STATE: California
;  COUNTRY: USA
;  ZIP: 94104
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/787,739
;  FILING DATE: 24-JAN-1997
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/485,049
;  FILING DATE: 07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/486,756
;  FILING DATE: 07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/477,504
;  FILING DATE: 07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/481,658
;  FILING DATE: 07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/485,862
;  FILING DATE: 07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/485,863
;  FILING DATE: 07-JUN-1995
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: US 08/487,077
;  FILING DATE: 07-JUN-1995
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Lauder, Leona L.
;  REGISTRATION NUMBER: 30,863
;  REFERENCE/DOCKET NUMBER: D-0021.4
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 415-981-0332
;  TELEFAX: 415-981-2034
;  INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 1522 base pairs
;  TYPE: nucleic acid
;  STRANDEDNESS: double
;  TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
;  ANTI-SENSE: NO
US-08-787-739-1

Query Match        100.0%;  Score 1522;  DB 3;  Length 1522;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy     61 CCTGCTCCAGGGCCTCACTGTGCAACTCGCTGCTGCTGCTTCTGATGCCTGTCCAT 120
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Qy    121 CCCGAGAGGTTGCCCCGGATGCAGGAGGAGGATTCCCCCTTGGGGAGGAGGAGGCTCTTCTCGGGGAA 180
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Qy    181 GATGACCCACTCGGGCGAGGAGGAGATCTCCCAGTGAAGAGGAGGAGGAGGAT 240
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Qy    301 GAAGTTAAGGCCTAAAATCAGAAGAAGGAGGGGCTCCCTGAAGTTAAGGATTCTACTGTT 360
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Db    361 GAGGCTTCCTGGGAGATCCTTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420

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Db    421 GACCAGAGTTCATTGCGGCTATGAGGGCGACACCCGCCCGCCCTGGCCCGGGTGTCCCCAGCCTGC 480

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Db    481 GCGGGCGCGCCGCTTCCAAGAGTCCACCGGTGGGATATCCCGCCCAGCTCAGTCCGCCGGGTCCC 540

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Db    601 AACAATGGGCACAGTGTGCAACTGAACCCTGCCTTCCAGCTCCCCGGCTCCCAGGTCCC 660

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Db    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTGTTCACCTCAGC 780

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Db    781 ACCGGCCTTTGCCAGAGTTGACGAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTGGCC 840

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Db    901 GAAGAAAATCGCTCAGAGAAGGCCTCAGAGACTCAGGGTCCCAGGAGGACTGGACATATCTGCACTC 960

Qy    901 GAAGAAAATCGCTCAGAGAAGGCCTCAGAGACTCAGGGTCCCAGGAGGACTGGACATATCTGCACTC 960
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Db    961 CTGCCCTCTGACTTCAGCCGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020

Qy    961 CTGCCCTCTGACTTCAGCCGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGTGTCATCTGGACGTGTTAACCAGACAGTGAGTGCTAAGCAGCTC 1080

Qy   1021 GCCCAGGGTGTCATCTGGACGTGTTAACCAGACAGTGAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCCTCTCTGACACCCTGTGGGGACCTGGTGACTCGAACTGAACTTCCGA 1140

Qy   1081 CACACCCCTCTCTGACACCCTGTGGGGACCTGGTGACTCGAACTGAACTTCCGA 1140
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Db   1141 GGCACGCAGCCGCCTTTGAAATGGGCGGAGTGATTGAGGGCCTCCCTCCCTGGACAGC 1200

Qy   1141 GGCACGCAGCCGCCTTTGAAATGGGCGGAGTGATTGAGGGCCTCCCTCCCTGGACAGC 1200
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Db   1201 AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCTCTGGCTGTGGCTGGCTGCTGGGTGACATCCTA 1260

Qy   1201 AGTCCTTCGGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCTCTGGCTGTGGCTGGCTGCTGGGTGACATCCTA 1260
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Db   1261 GCCCTGGTTTTTGGGCCCCCTTTTGCTGTCAGCTCACCGGCGGTCGGTGGTTCCTTGTTGTGCAGATGAGA 1320
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RESULT 6
US-08-487-077A-1

Sequence 1, Application US/08487077A
Patent No. 6069242
GENERAL INFORMATION:
  APPLICANT: Zavada, Jan
  APPLICANT: Pastorekova, Silvia
  APPLICANT: Pastorek, Jaromir
  TITLE OF INVENTION: MN Gene and Protein
  NUMBER OF SEQUENCES: 86
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Leona L. Lauder
  STREET: 6 Mariposa Court
  CITY: Tiburon
  STATE: California
  COUNTRY: USA
  ZIP: 94920
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/487,077A
  FILING DATE: 07-JUN-1995
  CLASSIFICATION: 514
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/260,190
  FILING DATE: 15-JUN-1994
  ATTORNEY/AGENT INFORMATION:
  NAME: Lauder, Leona L.
  REGISTRATION NUMBER: 30,863
  REFERENCE/DOCKET NUMBER: D-0021.3H
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-435-2034
  TELEFAX: 415-435-0727
  INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 1522 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: cDNA
  HYPOTHETICAL: NO
  ANTI-SENSE: NO

US-08-487-077A-1

Query Match 100.0%;   Score 1522;   DB 3;   Length 1522;
Best Local Similarity 100.0%;
Matches 1522;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy     1 ACAGTCAGCCGCATGGCTCCCCTGCCCCCAGCCCCTGGCTCCTCTGTTGATCCCGGCC   60
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Db     1 ACAGTCAGCCGCATGGCTCCCCTGCCCCCAGCCCCTGGCTCCTCTGTTGATCCCGGCC   60

Qy    61 CCTGCTCCAGGCCTTCACTGTGCAACTGCTGCTTCTTGATGCCTGCCAT  120
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Db    61 CCTGCTCCAGGCCTTCACTGTGCAACTGCTGCTTCTTGATGCCTGCCAT  120

Qy   121 CCCCAGAGTTGCCCCCGGATGCAGGAGGCAGGAGGATTCCCCTTGGGAGGA  180
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Db   121 CCCCAGAGTTGCCCCCGGATGCAGGAGGCAGGAGGATTCCCCTTGGGAGGA  180

Qy   181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGGA  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGGA  240

Qy   241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGATCTACCT  300
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Db   241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGATCTACCT  300

Qy   301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGATCTCCCTGAAGTTAGAGGAGGATCTACCTACTGTT  360
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Db   301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGGATCTCCCTGAAGTTAGAGGAGGATCTACCTACTGTT  360

Qy   361 GAGGCGTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACAGGGACAAAGAAGGAGGGGAT  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCGTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACAGGGACAAAGAAGGAGGGGAT  420

Qy   421 GACCAGAGTCATTGCGGCGTATGGAGGCGGACACCGCGCCCTGGCCCCGGGGTGTCCCCAGCCTGC  480
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Db   421 GACCAGAGTCATTGCGGCGTATGGAGGCGGACACCGCGCCCTGGCCCCGGGGTGTCCCCAGCCTGC  480

Qy   481 GCGGGCCCGCTTCCAGTCCCCGGGTGGAATATCGGCCCGCGCCCCCAGCTCGCCGCCTTCTGCCGCGC  540
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Db   481 GCGGGCCCGCTTCCAGTCCCCGGGTGGAATATCGGCCCGCGCCCCCAGCTCGCCGCCTTCTGCCGCGC  540

Qy   541 CTGCGCCCCCTGGGACTCCTGCGGCTTCCAGCTCCCGCCCGTCCCAGAACTGCGCCCTGCGC  600
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Db   541 CTGCGCCCCCTGGGACTCCTGCGGCTTCCAGCTCCCGCCCGTCCCAGAACTGCGCCCTGCGC  600

Qy   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGGCTAGAGATGGGCTCTGGGGTCCC  660
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Db   601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGGCTAGAGATGGGCTCTGGGGTCCC  660

Qy   661 GGGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGCGGCTGCCAGGTCGTCGTGGGGC  720
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Db   661 GGGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGCGGCTGCCAGGTCGTCGTGGGGC  720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTTCAGC  780
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Db   721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTTCAGC  780

Qy   781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGTCTCCGGCGCCGTGTTGGGCC  840
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Db   781 ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGGGTCTCCGGCGCCGTGTTGGGCC  840

Qy   841 GCCTTTCTGGAGGACGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTTCTCGGCCTTG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCCTTTCTGGAGGACGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGTTCTCGGCCTTG  900

Qy   901 GAAGAAAATCGGCTGAGGAGGCTCAGGACTCCAGGACTGGACATATCTGCACTC  960
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Db   901 GAAGAAAATCGGCTGAGGAGGCTCAGGACTCCAGGACTGGACATATCTGCACTC  960

Qy   961 CTGCCCTCTGACTTCAGCGCCGCTACTTCCAATATGAGGGTCTCTGACTACACCGCCCGTT  1020
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Db   961 CTGCCCTCTGACTTCAGCGCCGCTACTTCCAATATGAGGGTCTCTGACTACACCGCCCGTT  1020

Qy  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGTGCTAAGCAGCTC  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGTGCTAAGCAGCTC  1080

Qy  1081 CACACCCTTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGGCTACAGCTGAAACTTCCGA  1140
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Db  1081 CACACCCTTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGGCTACAGCTGAAACTTCCGA  1140

Qy  1261 GCCCTGGTTTTGGCCTTTTGCTGTCTCAAGGCGTCGCGGTTCCTGTGCAGATGAGA  1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GCCCTGGTTTTGGCCTTTTGCTGTCTCAAGGCGTCGCGGTTCCTGTGCAGATGAGA  1320

Qy  1321 AGGCAGCAGCAGGAGGGGAACCAAAAGGGGGTGTGAGCTACCGCCGAGAGGTAGCCGAG  1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGGCAGCAGCAGGAGGGGAACCAAAAGGGGGTGTGAGCTACCGCCGAGAGGTAGCCGAG  1380

Qy  1381 ACTGGAGCCTAGAGGCTGGGATCTTGGGAGAAATGTGAGAAGGCCACCACCCAGAGGCCATCTGACGG  1440
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Db  1381 ACTGGAGCCTAGAGGCTGGGATCTTGGGAGAAATGTGAGAAGGCCACCACCCAGAGGCCATCTGACGG  1440

Qy  1441 GGAGCCCGGTAACTGGTGTCCTGGCTCATTATGGCACTTCCTTTTTAACTGCCCAAGGAAAATT  1500
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Qy  1501 TTTTAAAATAAATATTTTATAAT  1522
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Db  1501 TTTTAAAATAAATATTTTATAAT  1522
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RESULT 7

US-08-485-863A-1

; Sequence 1, Application US/08485863A

; Patent No. 6093548

; GENERAL INFORMATION:

;   APPLICANT: Zavada, Jan
;   APPLICANT: Pastorekova, Silvia
;   APPLICANT: Pastorek, Jaromir
;   TITLE OF INVENTION: MN Gene and Protein
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Leona L. Lauder
;   STREET: 6 Mariposa Court
;   CITY: Tiburon
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94920
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: 514
;   CLASSIFICATION: 514
;   FILING DATE: 07-JUN-1995
;   APPLICATION NUMBER: US/08/485,863A
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/260,190
;   FILING DATE: 15-JUN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lauder, Leona L.
;   REGISTRATION NUMBER: 30,863
;   REFERENCE/DOCKET NUMBER: D-0021.3G
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-435-2034
;   TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1522 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO

US-08-485-863A-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[Nucleotide sequence alignment data: Query (Qy) and Database (Db) sequences aligned with matching bars, positions 1 through 1522]

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;     TELEPHONE:      415-981-2034
;     TELEFAX:        415-981-0332
; INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1522 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
; US-08-485-049D-1

Query Match        100.0%;   Score 1522;   DB 3;   Length 1522;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;  Conservative   0;  Mismatches   0;   Indels   0;   Gaps   0;

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Db      1 ACAGTCAGCCGCCATGGCTCCCCCTGTGCCCCAGCCCCTGCCCCTCTCCCTGTGATCCCGGCC 60

Qy     61 CCTGCTCCAGCCCTCACTGTGCAACTGCTGCTTCTGATGCCTCCAT 120
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Db     61 CCTGCTCCAGCCCTCACTGTGCAACTGCTGCTTCTGATGCCTCCAT 120

Qy    121 CCCCAGAGGTTGCCCCGGATGCAGCAGGAGGATTCCCCCTTGGGGGGGAA 180
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Db    121 CCCCAGAGGTTGCCCCGGATGCAGCAGGAGGATTCCCCCTTGGGGGGGAA 180

Qy    181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAGAGGAGGCTCTTCTGGGGGA 240
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Db    181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAGAGGAGGCTCTTCTGGGGGA 240

Qy    241 CCACCCGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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Db    241 CCACCCGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

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Db    301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGGCTCCCTGAAGTTAGAGGAGGATCTTACCTACTGTT 360

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAATAATGCCCACACAGGGACAAAAGAAGGGGAT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAATAATGCCCACACAGGGACAAAAGAAGGGGAT 420

Qy    421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGGCCCCCTGGCCCCCGGGTGTCCCCAGCCTGC 480
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Db    421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGGCCCCCTGGCCCCCGGGTGTCCCCAGCCTGC 480

Qy    481 GCGGGGCCGCTTCCAGTCCCCGGGTGGAATATCCGCCCCGGGCCCCTTCTGCCCGGGCC 540
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Db    481 GCGGGGCCGCTTCCAGTCCCCGGGTGGAATATCCGCCCCGGGCCCCTTCTGCCCGGGCC 540

Qy    541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGGCGCCCCAGAACTGCGCCTGCGC 600
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Db    541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGGCGCCCCAGAACTGCGCCTGCGC 600

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Db    601 AACAATGGCCACACAGTGTGCAAACTGACCCCTGCTTCTCGGGCTTAGAGATGCCTCTGGGTCCC 660

Qy    661 GGGCGGGAGGTACCCGGGCTCTGCAGGTCCTGCAGTTCGCAGTTCGCGGGC 720
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Db    661 GGGCGGGAGGTACCCGGGCTCTGCAGGTCCTGCAGTTCGCAGTTCGCGGGC 720

Qy    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGGATCCACGGTGGTTCACCTCAGC 780
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Db    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGGATCCACGGTGGTTCACCTCAGC 780

Qy    781 ACCCGCCTTTGCCCAGAGTTGACGAGGCCTTGGGGCGTGTTGGCC 840
          |||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACCCGCCTTTGCCCAGAGTTGACGAGGCCTTGGGGCGTGTTGGCC 840

Qy    961 CTGCCCTGACTTCAGCCGCTACTTCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGCCCTGACTTCAGCCGCTACTTCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT 1020

Qy   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGTGAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGTGAGTGCTAAGCAGCTC 1080

Qy   1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACACGTGACTTCCGA 1140
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Db   1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACACGTGACTTCCGA 1140

Qy   1141 GCGACGCAGCAGCCTTTGAATGGGCCAGTGATGATTGAGGGCCTCCTTCCCTTCCCTCCTG 1200
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Db   1201 AGTCCTCGGGCTGCTGAGGCCAGTCCAGCTGAATTCCTGCCTGGCTGGCTGCTGACATCCTA 1260

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Db   1261 GCCCTGGTTTTGGCCTCCTTTTTTTGCTGTCACCAGCGTCGCGGTTCCTTGTGTGCAGATGAGA 1320

Qy   1321 AGGCAGCACAGAGAGGGGAACCAAAGGGGGTGTGAGCTACGGCCCAGCAGAGGTAGCCCGAG 1380
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Db   1321 AGGCAGCACAGAGAGGGGAACCAAAGGGGGTGTGAGCTACGGCCCAGCAGAGGTAGCCCGAG 1380

Qy   1381 ACTGGGAGCCTAGAGGCTGGATCTTGGAGGAGAATGTGAGAAGCCAGAGGCATCTGAGGG 1440
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Db   1381 ACTGGGAGCCTAGAGGCTGGATCTTGGAGGAGAATGTGAGAAGCCAGAGGCATCTGAGGG 1440

Qy   1441 GGAGCCGGTAACTGTCCTGCTCATTATCCCACTTCCTTTTAACTGCCAAGAAATT 1500
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Qy   1501 TTTTAAATAAATATTTATAAT 1522
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Db   1501 TTTTAAATAAATATTTATAAT 1522
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RESULT 8
US-08-485-049D-1
; Sequence 1, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
;   APPLICANT: Zavada, Jan
;   APPLICANT: Pastorekova, Silvia
;   APPLICANT: Pastorek, Jaromir
;   TITLE OF INVENTION: MN Gene and Protein
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Leona L. Lauder
;   STREET: 369 Pine Street
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/485,049D
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/260,190
;   FILING DATE: 15-JUN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lauder, Leona L.
;   REGISTRATION NUMBER: 30,863
;   REFERENCE/DOCKET NUMBER: D-0021.3E
;   TELECOMMUNICATION INFORMATION:

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RESULT 9
US-09-178-115-1
; Sequence 1, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT: Zavada, Silvia
;  APPLICANT: Pastorek, Jaromir
;  APPLICANT: Pastorekova, Silvia
;  TITLE OF INVENTION: MN Gene and Protein
;  FILE REFERENCE: D-0021.5A
;  CURRENT APPLICATION NUMBER: US/09/178,115
;  CURRENT FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 09/177,776
;  EARLIER FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 08/787,739
;  EARLIER FILING DATE: 1997-01-24
;  EARLIER APPLICATION NUMBER: 08/485,049
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/486,756
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/477,504
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/481,658
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/485,862
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/485,863
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/487,077
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/260,190
;  EARLIER FILING DATE: 1994-06-15
;  EARLIER APPLICATION NUMBER: 08/177,093
;  EARLIER FILING DATE: 1993-12-30
;  EARLIER APPLICATION NUMBER: 07/964,589
;  EARLIER FILING DATE: 1992-10-21
;  EARLIER APPLICATION NUMBER: PV-709-92
;  EARLIER FILING DATE: 1992-03-11
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: Patentin Ver. 2.0
;
SEQ ID NO 1
;  LENGTH: 1522
;  TYPE: DNA
;  ORGANISM: HUMAN
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (13)..(1389)
;  FEATURE:
;  NAME/KEY: mat_peptide
;  LOCATION: (124)..(1389)
US-09-178-115-1

Query Match             100.0%;  Score 1522;  DB 3;  Length 1522;
Best Local Similarity   100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         1 ACAGTTCAGCGCGCAATGGCTCCCCTGTGCCCCAGCCCCTGCCTCCCTCGTTGATCCCGGCC    60
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Db         1 ACAGTTCAGCGCGCAATGGCTCCCCTGTGCCCCAGCCCCTGCCTCCCTCGTTGATCCCGGCC    60

Qy        61 CCTGCTCCAGGCCTCACTGTCGAACTGCTGCTTGCTGCTTCTCGATGCCTGTCGCAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCTGCTCCAGGCCTCACTGTCGAACTGCTGCTTGCTGCTTCTCGATGCCTGTCCAT   120

Qy       121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGGATTCCCCCTTGGGAGGAGGTCTTGGGGA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAGGATTCCCCCTTGGGAGGAGGTCTTGGGGA   180

Qy       181 GATGAACCCACTGGGCGCGAGGAGGAATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GATGAACCCACTGGGCGCGAGGAGGAATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT   240

Qy       241 CCACCCGGAGAGGAGGAGGATCTTACCTCGGAGGAGGAGGATCTACTTGGAGGAGGAGGATCTACCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CCACCCGGAGAGGAGGAGGATCTTACCTCGGAGGAGGAGGATCTACTTGGAGGAGGAGGATCTACCT   300

Qy       301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGAGTTAGATCTACCTGTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGAGTTAGATCTACCTGTT   360

Qy       361 GAGGCTCCTGGAGATCCTCAAGAACCCCACCAGGAGACCAGGAGGACAAAGAGAGGGGAT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GAGGCTCCTGGAGATCCTCAAGAACCCCACCAGGAGACCAGGAGGACAAAGAGAGGGGAT   420

Qy       421 GACCAGAGTTCATTGGCGCTATGGAGGCCGACCACCCCGTCCCCAGCCTGC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GACCAGAGTTCATTGGCGCTATGGAGGCCGACCACCCCGTCCCCAGCCTGC   480

Qy       481 GCGGGGCCGGCTTCCAGTCCCCGGTGGATATCCGCCCACCCCCCAGCCTGC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCGGGGCCGGCTTCCAGTCCCCGGTGGATATCCGCCCACCCCCCAGCCTGC   540

Qy       541 CTGCGCCCCCCTGGAACTCCTGGGCTTCCAGCTCCCCAGAACTGCGCCCCTGGGC   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 CTGCGCCCCCCTGGAACTCCTGGGCTTCCAGCTCCCCAGAACTGCGCCCCTGGGC   600

Qy       601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGGCTGAGATGGCTCTGGGTCCC   660
```

(Alignment continues — detailed base-by-base matching between Qy (query) and Db (database) sequences from position 1 through 1522.)

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCTCTTCCTTGTTGATCCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCCGCCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCTCTTCCTTGTTGATCCCGGCC 60

Qy     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTCGTCAGCTGCTTCTGATCGCCTTCCAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCTCCAGGCCTCACTGTGCAACTGCTCGTCAGCTGCTTCTGATCGCCTTCCAT 120

Qy    121 CCCCAGAGGTTGCCCCGGACGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGAGGTTGCCCCGGACGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCGGGAA 180

Qy    181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGAGGAGGAT 240

Qy    241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACCCGGAGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Qy    301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGGAGCCTACTGTT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGGCTCCCTGAAGTTAGAGGGAGCCTACTGTT 360

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGGCTCCTGGAGATCCTCAAGAGACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
```

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Db    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601                                                                660

Db    661 GGGCGGGAGTACCGGGGGCTCTGCAGCTGCATCTGCAGCTGGGGGGGTCTCTCCGGGC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661                                                            720

Db    721 TCGGAGCACACGTGTGGAAGGGCCACACGGTTTCCCTGCCCGGGATCCACGTGGTTCACCTCAGC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721                                                               780

Db    781 ACCGCCCTTGCCAGAGTTGACGAGGCCCTTGGGGGCCCTGGGGCCGGTGTGTTGGCC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781                                                            840

Db    841 GCCTTTCTTGGAGGAGGGCCCCGGGAAGAAAACAGTGGGGGGGGGGGGGGGCCTGGCCTTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841                                                            900

Db    901 GAAGAAATCGGCTGAGGAAGGGCTCAGAGACTCAGGTCCCAGGGACTGGACATATCTGCACTC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901                                                            960

Db    961 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCCTGT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961                                                           1020

Db   1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGTGCTAAGCAGCTC
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021                                                        1080

Db   1081 CACACCCTTCTCTGACACCCTGTGGGGACTCGGCTACAGCTGAACTTCCGA
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081                                                   1140

Db   1141 GCGACGCAGCCTTTGAAATGGGCGAGTGATTGAGGCCCTCCTTCCCGTTCCCGTTGGAGTGGACAGC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141                                                              1200

Db   1201 AGTCCTCCGGGCTCCGGCTCCAGCTGAAATTCCTGGCTGCTGGTGACATCCTA
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201                                                     1260

Db   1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGGCGGTCCGGTTCCTTGGTCAGATGAGA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261                                                          1320

Db   1321 AGGCAGCACAGGAGGGGGAACCAAAGGGGGTGTGAGCTACCGGCCGCCCAGCGACGAGAGGTAGCGGAG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321                                                                1380

Db   1381 ACTGGAGCCCTAGAGGCTTGGATCTTGGAGAAATGTGAGAGAGGGCCATCTGAGGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381                                                       1440

Db   1441 GGAGCCGGTAACTGTCTGTCCTGCTCATTATGCCACTTCCTTTAACTGCCAAGAAATT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441                                                         1500

Db   1501 TTTTAAAATAAATATATTTATAAT
          ||||||||||||||||||||||||
Qy   1501 TTTTAAAATAAATATATTTATAAT 1522
```

RESULT 11
US-09-772-719B-1
; Sequence 1, Application US/09772719B
; Patent No. 677O438
; GENERAL INFORMATION:
; APPLICANT:
;   Zavada, Jan
;   Pastorekova, Silvia
;   Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719B
; FILING DATE: 30-Jan-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-772-719B-1

Query Match   100.0%;   Score 1522;   DB 4;   Length 1522;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 60

Qy   61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTTCACTGCTGATGCCGTGTCCAT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTTCACTGCTGATGCCGTGTCCAT 120

Qy   121 CCCCAGGAGGTTGCCCCCGGATGCGAGGAGGATTCCCCCCTTGGGAGGAGGCCTTCTG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCCAGGAGGTTGCCCCCGGATGCGAGGAGGATTCCCCCCTTGGGAGGAGGCCTTCTG 180

Qy   181 GATGACCCACTGGGCGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATGACCCACTGGGCGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 240

Qy   241 CCACCCGGAGGAGGATCTACCTGGAGAGGAGGAGGATCTACCT 300

[Alignment continues — Qy (query) and Db (database) paired lines from position 421 through 1522, full identity match across the sequence]

RESULT 12
US-08-260-190-5
; Sequence 5, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-08-260-190-5

Query Match   100.0%; Score 1522; DB 4; Length 1522;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACAGTTCAGCGCGCATGGCTGCTCCCCGTGCCCCAGCCCTCCCTGTTGATCCCGGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACAGTTCAGCGCGCATGGCTGCTCCCCGTGCCCCAGCCCTCCCTGTTGATCCCGGCC 60

Qy   61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCGTGATGCCGTCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTTCGTGATGCCGTCCAT 120

Qy   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGC 180
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCTTGGGAGGAGGC 180

Qy   181 GATGACCCACTGGGCGGAGGAGGATTCGCCCAGTGAAAGAGAGGAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATGACCCACTGGGCGGAGGAGGATTCGCCCAGTGAAAGAGAGGAGGAT 240

Qy   241 CCACCCGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
              |||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACCCGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Qy   301 GAAGTTAAGCTAAATCAGAAGAACAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAAGTTAAGCTAAATCAGAAGAACAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 360

Qy   241 CCACCCCGAGAGGAGGGATCTACCTGGAGGAGGATCTACCT 300

```
RESULT 13
US-08-260-190-23
; Sequence 23, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT: Pastorekova, Silvia
;  APPLICANT: Pastorek, Jaromir
;  TITLE OF INVENTION: MN Gene and Protein
;  FILE REFERENCE: D-0021-2
;  CURRENT APPLICATION NUMBER: US/08/260,190A
;  CURRENT FILING DATE: 1994-06-15
;  EARLIER APPLICATION NUMBER: 08/177,093
;  EARLIER FILING DATE: 1993-12-30
;  EARLIER APPLICATION NUMBER: 07/964,589
;  EARLIER FILING DATE: 1992-10-21
;  EARLIER APPLICATION NUMBER: PV-709-92
;  EARLIER FILING DATE: 1992-03-11
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
;  LENGTH: 5052
;  TYPE: DNA
;  ORGANISM: HUMAN
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)..(5052)
US-08-260-190-23
```

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Query Match 93.1%; Best Local Similarity 99.3%; Score 1416.8; DB 4; Length 5052;
Matches 1506; Conservative 0; Mismatches 0; Pred. No. 0; Indels 8; Gaps 8;
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Qy      10 CGCATGGGCTCCCGTTGCCCGCCCAGCCCTGGCTCCTCTGTTGTTGATCCCCGCGCCCTGCTCCA 69
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3542 CGCATGGGCTCCCGTTGCCCGCCCAGCCCTGGCTCCTCTGTTGTTGATCCCCGCGCCCTGCTCCA 3601

Qy      70 GGGCTCACTGTGCAACTGCTGCTGTTCACTGCGTGCTTCTGATGCTGTCCATCCCCAGAGG 129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3602 GGGCTCACTGTGCAACTGCTGCTGTTCACTGCGTGCTTCTGATGCCTGTCCATCCCCAGAGG 3661

Qy     130 TTTGCCCCGGATGCGAGGAGGATTCCCCTTGGGGAAGAGCTCTTCTCGGGAAGAGATGACCCA 189
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3662 TTGCCCCCGGATGCGAGGAGGATTCCCCTTT-GGAGGAGGCTCTTCTCGGGAAGATGACCGA 3720

Qy     190 CTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGAGGATCCAGAGGAGGAGGAGGATCCACCCGGA 249
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 CTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGAGGATCACCCAGAGGAGGAGGAGGATCCACCCGGA 3780

Qy     250 GAGGAGGATCTACCTGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGTTAAT- 308
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 GAGGAGGATCTACCTGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGAAGTTAAT 3840

Qy     309 GCCTAAATCAGAAGAGAAGAGAGGGCTCCCTGAAGTTAGAGAGATCTACCTACTGTTGAGGCTCC 368
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 GCCTAAATCAGAAGAGAAGAGAGGGCTCCCTGAAGTTAGAGAGATCTACCTACTGTTGAGGCTCC 3900

Qy     369 TGGAGATCCTCAAGAACCCCAGAATAATGCCACAGGGACAAAGAAGGGACCAGAG 428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 TGGAGATCCTCAAGAACCCCAGAATAATGCCACAGGGACAAAGAAGGGACCAGAG 3960

Qy     429 TCATTGCGCTATGGAGCGGACCCCGCCCCTGGCCCCGGTGTCCCCCAGCCCTGCGCGGGCG 488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         TCATTGCGCTATGGAGCGGACCCCGCCCCTGGCCCCGGTGTCCCCCAGCCCTGCGCGGGCG
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```
RESULT 14
US-08-335-469-1
Sequence 1, Application US/08354469A
; Patent No. 6004535
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide
; TITLE OF INVENTION: Using MN-Specific Antibodies
; FILE REFERENCE: D-0021A
; CURRENT APPLICATION NUMBER: US/08/335,469A
; CURRENT FILING DATE: 1994-11-07
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-335-469-1
```

```
Query Match          91.9%;  Score 1399;  DB 3;  Length 1399;
Best Local Similarity 100.0%;  Pred. No. 0;  Indels 0;  Gaps 0;
Matches 1399;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy  124 CAGAGGTTGCCCGGATGCAGGAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAAGAT 183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CAGAGGTTGCCCGGATGCAGGAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAAGAT 60

Qy  184 GACCCCACTGGGCGCGAGGAGGATCTCCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCA 243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GACCCCACTGGGCGCGAGGAGGATCTCCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCA 120

Qy  244 CCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGAA 303
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGAA 180

Qy  304 GTTAAGCCTAAATCAGAAGAAGAGAGGGGTCCCCTGAAGTTAGGAGGATTAGAGGATTGAG 363
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GTTAAGCCTAAATCAGAAGAAGAGAGGGGTCCCCTGAAGTTAGGAGGATTAGAGGATTGAG 240

Qy  364 GCTCCTGGAGATCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAAGAGGGGATGAC 423
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GCTCCTGGAGATCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAAGAGGGGATGAC 300

Qy  424 CAGAGTCAATGGGCGCTATGGAGGAGGGACCGGACCGGCGGTCCCCAGCCTGGCGG 483
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CAGAGTCAATGGGCGCTATGGAGGAGGGACCGGACCGGCGGTCCCCAGCCTGGCGG 360

Qy  484 GGCCGCTTCCAGTCCCCGGTGGATATCCGCGCCCCCGGGGGTCCCGGCCTCTTCGCCGGGCAAC 543
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GGCCGCTTCCAGTCCCCGGTGGATATCCGCGCCCCCGGGGGTCCCGGCCTCTTCGCCGGGCAAC 420

Qy  544 CGCCCCTCGGAACTCCTGGGCTTCCAGCTGCCCGCCCCGCGGTTCGCGGGCGCCCTG 603
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CGCCCCTCGGAACTCCTGGGCTTCCAGCTGCCCGCCCCGCGGTTCGCGGGCGCCCTG 480

Qy  604 AATGGCCACAGTGTGCAACTGACCCCTGCCTCTCCGCCCTGCGCCAGTCCTCGGGCTCG 663
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AATGGCCACAGTGTGCAACTGACCCCTGCCTCTCCGCCCTGCGCCAGTCCTCGGGCTCG 540

Qy  664 CGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGCTCGGCAGGTCGTCCGGGCTCG 723
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGCTCGGCAGGTCGTCCGGGCTCG 600

Qy  724 GAGCACACGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGGTTCACCTCAGCACC 783
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GAGCACACGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGGTTCACCTCAGCACC 660
```

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Qy  789 TGCCAGAGTTGACGAGGGCCTTGGGGGGCCCGGGGGGGGCCTGGCCGTGTTGGCCGGCTTTTCT 848
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  729 CACTGTGAAAGGCGCACCGTTTCCTGCCGAGATCCACGTGGTTCACCTCACGCACCGCCTT 788

Qy  849 GGAGGAGGGCCCGGAAGAAGAAAACAGTG-CCTATGAGGCAGTTGTGTCTGTGTCTGCCTTGGAAGAAA 907
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4258 CACTGTGGAGAAGGCCACCGTTTCCTGCCGAGATCCACGTGGTTCACCTCAGCACCGCTT 4317

Qy  908 TCCCTGAGGAAGGCTTCAGAGACTCAGGTCCCAGGGCTCCCAGAACTGAGCATTTCTCTGCCCT 967
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4318 TGCCAGAGTTGACGAGGGCCTTGGGGGGCCCGGGGGGGGCCTGGCCGTGTTGGCCGGCTTTTCT 4376
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Qy 4377 GGAGGAGGGGCCCGGAAGAAGAAAACAGTGTCCTATGAGGCAGTTGTGTCTGTGTCTGCCTTGGAAGAAA 4436
Db  849 GGAGGAGGGCCCGGAAGAAGAAAACAGTG-CCTATGAGGCAGTTGTGTCTGTGTCTGCCTTGGAAGAAA 907

Qy 4497 CTGACTTCAGCGCCTACTTCCAATATGAGGGGTTCTCGACTACACCGCGCCCTGTGCCCAGG 4556
Db  968 CTGACTTCAGCGCCTACTTCCAATATGAGGGGTTCTCGACTACACCGCGCCCTGTGCCCAGG 1027

Qy 4557 GTGTCATCTGGGACTGTGTTTAAACGAGACAGTGATGCTGAGTGCTAAGCAGCTCCACACC 4616
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RESULT 15
US-08-260-190-1

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;  Sequence 1, Application US/08260190A
;  Patent No. 6774117
;  GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT: Pastorekova, Silvia
;  APPLICANT: Pastorek, Jaromir
;  TITLE OF INVENTION: MN Gene and Protein
;  FILE REFERENCE: D-0021-2
;  CURRENT APPLICATION NUMBER: US/08/260,190A
;  CURRENT FILING DATE: 1994-06-15
;  EARLIER APPLICATION NUMBER: 08/177,093
;  EARLIER FILING DATE: 1993-12-30
;  EARLIER APPLICATION NUMBER: 07/964,589
;  EARLIER FILING DATE: 1992-10-21
;  EARLIER APPLICATION NUMBER: PV-709-92
;  EARLIER FILING DATE: 1992-03-11
;  NUMBER OF SEQ ID NOS: 26
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US-08-260-190-1
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OM nucleic - nucleic search, using sw model

Run on: February 6, 2005, 03:56:53 ; Search time 860 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Searched:　　4300275 seqs, 2872944193 residues

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2	1522	100.0	1522	10	US-09-967-237-1	Sequence 1, Appli
3	1522	100.0	1522	15	US-10-795-933-5	Sequence 5, Appli
4	1522	100.0	1522	18	US-10-888-694-1	Sequence 1, Appli
5	1522	100.0	1552	9	US-09-954-456-89	Sequence 89, Appl
6	1522	100.0	1552	9	US-09-954-456-726	Sequence 726, App
7	1522	100.0	1552	10	US-09-960-706-1080	Sequence 1080, Ap
8	1522	100.0	1552	10	US-09-873-367C-516	Sequence 516, App
9	1522	100.0	1552	11	US-09-968-007A-213	Sequence 213, App
10	1522	100.0	1552	15	US-10-301-822-11	Sequence 11, Appl
11	1522	100.0	1552	15	US-10-465-57-9	Sequence 9, Appli
12	1522	100.0	1552	15	US-10-172-118-574	Sequence 574, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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14	1522	100.0	1552	15	US-10-295-027-305	Sequence 305, App
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16	1522	100.0	1552	16	US-10-734-564-71	Sequence 71, Appl
17	1522	100.0	1552	17	US-09-772-719-28	Sequence 28, Appl
18	1522	100.0	1658	18	US-10-723-860-460	Sequence 460, App
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26	414.4	27.2	415	9	US-09-772-719-28	Sequence 28, Appl
27	413.4	27.2	445	10	US-09-967-237-28	Sequence 28, Appl
28	413.4	27.2	445	18	US-10-888-694-28	Sequence 28, Appl
29	413.4	27.2	331	16	US-10-242-535A-11940	Sequence 11940, A
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31	331	21.7	304	16	US-09-777-564-348	Sequence 348, App
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36	296	19.4	305	15	US-10-102-524-697	Sequence 697, App
37	293	19.3	305	9	US-09-777-564-8	Sequence 8, Appli
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RESULT 1
US-09-772-719-1
Sequence 1, Application US/09772719
Patent No. US20020137910A1

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-JAN-2001
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E

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;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-981-2034
;     TELEFAX: 415-981-0332
;  INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH: 1522 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
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US-09-772-719-1

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GAAGAAAATCGGCTGAGGAAGGGCTCAGAGGAGGCTCAGGTCCCAGGGACTGGACAGTTGGCTGCACTC 960

Qy    961 CTGCCCTCCTGACTTCAGCGCGCCTACTTCCAATATGAGGGGGTCTTCTGACTACCACCGCCCTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTGCCCTCCTGACTTCAGCGCGCCTACTTCCAATATGAGGGGGTCTTCTGACTACCACCGCCCTGT 1020

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080

Qy   1081 CACACCCCTCTCTGACACCCTGTGGGGGACCTGGTTGACTTCTCGGCGCTACAGCTGAACTTCCGA 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CACACCCCTCTCTGACACCCTGTGGGGGACCTGGTTGACTTCTCGGCGCTACAGCTGAACTTCCGA 1140

Qy   1141 GCGACGCAGCCTTTGAATGGGGCGGAGTGAGTGACTTGAGGGTCCCTCCTTCCCGTCCGGAGTGGGACAGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCGACGCAGCCTTTGAATGGGGCGGAGTGAGTGACTTGAGGGTCCCTCCTTCCCGTCCGGAGTGGGACAGC 1200

Qy   1201 AGTCCTCGGGCTGCCTGACCCAGTCCAGTTCCTCCTGCCTGCTCCTGCTGGGTGACATCCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGTCCTCGGGCTGCCTGACCCAGTCCAGTTCCTCCTGCCTGCTCCTGCTGGGTGACATCCTA 1260

Qy   1261 GCCCTGGTTTTTTGGGCCTCCTTTTTGCTGTCACCAGCGGTCGCGTTCCTTGTTGTGCAGATGGA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCTGGTTTTTTGGGCCTCCTTTTTGCTGTCACCAGCGGTCGCGTTCCTTGTTGTGCAGATGGA 1320

Qy   1321 AGGCAGCACAGAAGGGAGGACCAAAAGGGGGGTTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGGCAGCACAGAAGGGAGGACCAAAAGGGGGGTTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380

Qy   1381 ACTGGAGCCTAGAGGCTGGGATCTTGGAGAAATGTGAGAAGGCCAGCCCAGAGGGCATCTGAGGG 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACTGGAGCCTAGAGGCTGGGATCTTGGAGAAATGTGAGAAGGCCAGCCCAGAGGGCATCTGAGGG 1440

Qy   1441 GGAGCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTTTAACTGCCAAGAAATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GGAGCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTTTAACTGCCAAGAAATT 1500

Qy   1501 TTTTAAAATAAAATAATTTTATAAT 1522
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Db   1501 TTTTAAAATAAAATAATTTTATAAT 1522
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;         NAME/KEY: mat_peptide
;         LOCATION: (124)..(1389)
US-09-967-237-1

Query Match             100.0%;  Score 1522;  DB 10;  Length 1522;
Best Local Similarity   100.0%;  Pred. No. 0;  Mismatches 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ACAGTCAGCGAGCCGATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGGATCCGGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ACAGTCAGCGAGCCGATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGGATCCGGCC 60

Qy     61 CCTGCTCTCAGGCCCTCACTGTTGCAACTGTTGCTGTTCTGATGCCTGTCCAT 120
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Db     61 CCTGCTCTCAGGCCCTCACTGTTGCAACTGTTGCTGTTCTGATGCCTGTCCAT 120
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(sequence alignment continues, Query vs Database, 100% match, positions 1–1522)

Query Match 100.0%; Score 1522; DB 18; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     1 ACAGTTCAGCGCGACATGGCTCACTGTGTCCCCGTGTCCCCAGCCCTGCTCCCTCTTGTGTTGATCCCCGCC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ACAGTTCAGCGCGACATGGCTCACTGTGTCCCCGTGTCCCCAGCCCTGCTCCCTCTTGTGTTGATCCCCGCC 60

Qy    61 CCTTGCTCCAGGGCCTCACTGTGTCGCAACTGCTGCTTCTCGAGCCTGTCCAT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCTGCTCCAGGGCCTCACTGTGTCGCAACTGCTGCTTCTCGATGCCTGTCCAT 120

Qy   121 CCCCAGAGGTTGCCCGGGATGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTTCTGGGGGAA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCCAGAGGTTGCCCGGGATGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTTCTGGGGGAA 180

Qy   181 GATGACCCACTGGGCGACGAGGAGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAGGAT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GATGACCCACTGGGCGACGAGGAGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAGGAT 240

Qy   241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
         ||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300

Qy   301 GAAGTTAAGCCTAAATCAGAAGAAGAGGAGGCTCCCCTGAAGTTAGAGGATCTACCTACTGTT 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAAGTTAAGCCTAAATCAGAAGAAGAGGAGGCTCCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Qy   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420

Qy   421 GACCAGAGTCATTGGGCGTATGGAGGGCGACCCCGCCCCGGGGTGTCCCCAGCCCTGC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GACCAGAGTCATTGGGCGTATGGAGGGCGACCCCGCCCCGGGGTGTCCCCAGCCCTGC 480

Qy   481 GCGGGCCGCTTCCAGTCCCGGTGGATATCCGGCCCGCCCCTTCGCCCCGCC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GCGGGCCGCTTCCAGTCCCGGTGGATATCCGGCCCGCCCCTTCGCCCCGCC 540

Qy   541 CTGCGCCCCCCTGGAACTCCTGGGCTTCAGCTCCCGGTGCCCCTGCGC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGCGCCCCCCTGGAACTCCTGGGCTTCAGCTCCCGGTGCCCCTGCGC 600

Qy   601 AACAATGGCCACCAGTGTGCACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACAATGGCCACCAGTGTGCACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCC 660

Qy   661 GGGGCGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGTGGTGGTCCGGGGC 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGGGCGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGGGGTGGTGGTCCGGGGC 720

Qy   721 TCGGAGCACACTGTGGAAGGCCACCACCGTTTCCCGCGGAATCCAGCGTGGTTCAACCTCAGC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCGGAGCACACTGTGGAAGGCCACCACCGTTTCCCGCGGAATCCAGCGTGGTTCAACCTCAGC 780

Qy   781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCCCTGGGCGGAGGCCTGGGCCTTGGGGGCC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCCCTGGGCGGAGGCCTGGGCCTTGGGGGCC 840

Qy   841 GCCTTTCTGGAGGAGGGGGCCCGGAAGAAAAACAGTGCCTATGAGGAGTTGCTGTGTCGGTTG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GCCTTTCTGGAGGAGGGGGCCCGGAAGAAAAACAGTGCCTATGAGGAGTTGCTGTGTCGGTTG 900

Qy   901 GAAGAAATCGCTCAGGAAGGCTCAGGTCCCAGGACTTGGTTGGACATATCTGCACTC 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GAAGAAATCGCTCAGGAAGGCTCAGGTCCCAGGACTTGGTTGGACATATCTGCACTC 960

Qy   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACACCGCCCTGT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CTGCCCTCTGACTTCAGCGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACACCGCCCTGT 1020

Qy  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAGCAGTGAGTGCTGAGTGCTAAGCAGCTC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAGCAGTGAGTGCTGAGTGCTAAGCAGCTC 1080

Qy  1081 CACACCCTCTGACACCCCTGTGGGGACCTGGTGACTGCTGGGGGAACCTGGTGACTGCTTCCGA 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CACACCCTCTGACACCCCTGTGGGGACCTGGTGACTGCTGGGGGAACCTGGTGACTGCTTCCGA 1140

Qy  1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200

Qy  1201 AGTCCTCGGGGCTGCTGAGCCGTCCAGCTGAATTCCTGCCTGGTGGTGCTGGTGGTGACATCCTA 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AGTCCTCGGGGCTGCTGAGCCGTCCAGCTGAATTCCTGCCTGGTGGTGCTGGTGGTGACATCCTA 1260

Qy  1261 GCCCTGGTTTTTGGCCCTCCTTTTTGCTGTCCACCAGCGTGGTCGCGGTTCCTTGTGCAGATGAGA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GCCCTGGTTTTTGGCCCTCCTTTTTGCTGTCCACCAGCGTGGTCGCGGTTCCTTGTGCAGATGAGA 1320

Qy  1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTAGCCCGAG 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGGTGTGAGCTACCGGCCCAGCAGAGGTAGCCCGAG 1380

Qy  1381 ACTGGAGCCTAGGACTGGATCTTGGGAGAATGTGAGAAGCCAGCAGAGACATCTGAGGG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 ACTGGAGCCTAGGACTGGATCTTGGGAGAATGTGAGAAGCCAGCAGAGACATCTGAGGG 1440

Qy  1441 GGAGCCGGTAACTGTCCTGCTCCGCTCATTATCGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GGAGCCGGTAACTGTCCTGCTCCGCTCATTATCGCCACTTCCTTTTTAACTGCCAAGAAATT 1500

Qy  1501 TTTTAAAATAAATAAATATTTATAAT 1522
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Db  1501 TTTTAAAATAAATAAATATTTATAAT 1522
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;   TELEPHONE: 415-981-2034
;   TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1522 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-888-694-1

Query Match      100.0%;  Score 1522;  DB 18;  Length 1522;
Best Local Similarity  100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy       1 ACAGTCAGCCGCATGGCTCCCCTGTCCCCAGCCCCTGGCCTCCCTCTGTTTGATCCCGGCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ACAGTCAGCCGCATGGCTCCCCTGTCCCCAGCCCCTGGCCTCCCTCTGTTTGATCCCGGCC 60

Qy      61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTTCTGATGCCTGTGTCCAT 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTTCTGATGCCTGTGTCCAT 120

Qy     121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATCAGGAGGATCTCTTCTGGGGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATCAGGAGGATCTCTTCTGGGGAA 180

Qy     181 GATGACCCACTGGGCGGACGAGGATCTGCCCAGTGAAGAGGAGGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GATGACCCACTGGGCGGACGAGGATCTGCCCAGTGAAGAGGAGGAT 240

Qy     241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300
           |||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT 300

Qy     301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGCTCCCTGAAGTTAGGAGGAT 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GAAGTTAAGCCTAAATCAGAAGAAGAGAGGGCTCCCTGAAGTTAGGAGGAT 360

Qy     361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCACAGGGAGGGAT 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCACAGGGAGGGAT 420

Qy     421 GACCAGAGTCATTGGGCTATGGAGGGACCCGCCTGGCCTGC 480
           |||||||||||||||||||||||||||||||||||||||||
Db     421 GACCAGAGTCATTGGGCTATGGAGGGACCCGCCTGGCCTGC 480

Qy     481 GCGGGGCCGCTTCCAGTCGGAATATCCGCCCAGCTCCTGCCCGGC 540
           |||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGGGGCCGCTTCCAGTCGGAATATCCGCCCAGCTCCTGCCCGGC 540

Qy     541 CTGCGCCCCCTGGAACTCCTGGGCTTCAGCTCCCAGAACTGCGCCCTGCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CTGCGCCCCCTGGAACTCCTGGGCTTCAGCTCCCAGAACTGCGCCCTGCC 600

Qy     601 AACAATGGCCACAGTGTGCAACTGAACCCTGGGCCTAGAGATGGCTCTGGGGTCCC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACAATGGCCACAGTGTGCAACTGAACCCTGGGCCTAGAGATGGCTCTGGGGTCCC 660

Qy     661 GGGCGGGAGTACCGGGGCTCTGCAGCTGGGGGCTGCAGGTCGTCCGGGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GGGCGGGAGTACCGGGGCTCTGCAGCTGGGGGCTGCAGGTCGTCCGGGC 720

Qy     721 TCGGGAGCACACTGTGGAAGGGCCACCGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TCGGGAGCACACTGTGGAAGGGCCACCGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780

Qy     781 ACCGCCCTTTGCCAGAGTTGACGAGGGCCTTGGGCGGCCCGGGGAGGCCTTGGCCGTTGTTGGCC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ACCGCCCTTTGCCAGAGTTGACGAGGGCCTTGGGCGGCCCGGGGAGGCCTTGGCCGTTGTTGGCC 840

Qy     841 GCCTTTCTGGAGGAGGGGCCCGGGAGGAGAAAACAGTTGCCTATGAGCAGTTGCTTG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GCCTTTCTGGAGGAGGGGCCCGGGAGGAGAAAACAGTTGCCTATGAGCAGTTGCTTG 900

Qy     901 GAAGAAATCGGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGAGACTGGACATATCTGCACTC 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GAAGAAATCGGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGAGACTGGACATATCTGCACTC 960

Qy     961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATACAGGGGTTCTTGACTACACCGCCCTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATACAGGGGTTCTTGACTACACCGCCCTGT 1020

Qy    1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGATACAGTGATGCTTAAGCAGCTC 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGATACAGTGATGCTTAAGCAGCTC 1080

Qy    1081 CACACCCTCTTCGACACCCTGTGGGGGACCTGGGTGACTCTCGGGGCTACAGCTTCCGA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CACACCCTCTTCGACACCCTGTGGGGGACCTGGGTGACTCTCGGGGCTACAGCTTCCGA 1140

Qy    1141 GCGACGCAGCCTGTTTGAAATGGGCGGAGTGGAGTGTGATTGAGTGACAGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GCGACGCAGCCTGTTTGAAATGGGCGGAGTGGAGTGTGATTGAGTGACAGC 1200

Qy    1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCGGGCTGACATCCTA 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAAATTCCTGCGGGCTGACATCCTA 1260

Qy    1261 GCCCTGGTTTTGGCCTCCTTTTGCTGTCACCAGCGTCGGGTTCCTGTTCAGATGAGA 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GCCCTGGTTTTGGCCTCCTTTTGCTGTCACCAGCGTCGGGTTCCTGTTCAGATGAGA 1320

Qy    1321 AGGGCAGCACAGAGAGGGGACCAAAGGGGGTGTTGGAGCGTTACGGGCCGAGGGTACCGAG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AGGGCAGCACAGAGAGGGGACCAAAGGGGGTGTTGGAGCGTTACGGGCCGAGGGTACCGAG 1380

Qy    1381 ACTGGAGCCTAGAGGCTGAATCTTGGAGAAGTGAGAAGCCAGAGGCATCTGAGGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 ACTGGAGCCTAGAGGCTGAATCTTGGAGAAGTGAGAAGCCAGAGGCATCTGAGGG 1440

Qy    1441 GGAGCCGGTAACTGTCCTGTCCTGTCATTATGCCAACTTCCTTTTAACTGCCAAGAAATT 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GGAGCCGGTAACTGTCCTGTCCTGTCATTATGCCAACTTCCTTTTAACTGCCAAGAAATT 1500

Qy    1501 TTTTAAAAATAAATATTTATATAT 1522
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Db    1501 TTTTAAAAATAAATATTTATATAT 1522
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RESULT 5
US-09-954-456-89
;  Sequence 89, Application US/0954456
;  Patent No. US20020115057A1
; GENERAL INFORMATION:
;   APPLICANT: Young, Paul
;   TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;   TITLE OF INVENTION: Sets
;   FILE REFERENCE: 689290-76
;   CURRENT APPLICATION NUMBER: US/09/954,456
;   CURRENT FILING DATE: 2001-09-18
;   PRIOR APPLICATION NUMBER: US/60/233,617
;   PRIOR FILING DATE: 2000-09-18
;   PRIOR APPLICATION NUMBER: US/60/234,052
;   PRIOR FILING DATE: 2000-09-20
;   PRIOR APPLICATION NUMBER: US/60/234,923
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,134
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,637
;   PRIOR FILING DATE: 2000-09-26
;   PRIOR APPLICATION NUMBER: US/60/235,638
;   PRIOR FILING DATE: 2000-09-26
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Query Match        100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy    1  ACAGTCAGCCGCACATGGCTCCCCGTGCCCCCAGCCCCTCGTTGCCCTCTCTGTTGATCCCCGCC   60
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Db   31  ACAGTCAGCCGCACATGGCTCCCCGTGCCCCCAGCCCCTCGTTGCCCTCTCTGTTGATCCCCGCC   90
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(DNA sequence alignment — query "Qy" aligned to database "Db", continuing in 60-base increments through position 1552)

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;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: Patentin version 3.0
;
;  SEQ ID NO 726
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  LENGTH: 1552

US-09-954-456-726

Query Match        100.0%;  Score 1522;  DB 9;  Length 1552;
Best Local Similarity  100.0%;
Matches 1522;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       1  ACAGTCAGCGCCATGGCTTCCCCGTTCCCCTTGTGCCCCAGCCCTGGCTCCTCCTCTTGTTGGATCCCGGCC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1  ACAGTCAGCGCCATGGCTTCCCCGTTCCCCTTGTGCCCCAGCCCTGGCTCCTCCTCTTGTTGGATCCCGGCC  60

Qy      61  CCTGCTCCAGGGCCTCACTGTCGCACTGCTGCTGTCACTGCCTTCTCGATGCCTGTCCAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  CCTGCTCCAGGGCCTCACTGTCGCACTGCTGCTGTCACTGCCTTCTCGATGCCTGTCCAT  120

Qy     121  CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTTCTGGGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTTCTGGGAA  180

Qy     181  GATGACCCACTGGGCGACGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGAGGAGGAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  GATGACCCACTGGGCGACGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT  240

Qy     211  GATGACCCACTGGGCGACGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT  270
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211  GATGACCCACTGGGCGACGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT  270

Qy     241  CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT  300
            ||||||||||||||||||||||||||||||||||||||||||||
Db     271  CCACCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCT  330

Qy     301  GAAGTTAAGCCTAAAATCAGAGAAGAGGAGGCTCTCCTGAAGTTAGAGGATCTACTACTGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  GAAGTTAAGCCTAAAATCAGAGAAGAGGAGGCTCTCCTGAAGTTAGAGGATCTACTACTGTT  390

Qy     331  GAAGTTAAGCCTAAAATCAGAGAAGAGGAGGCTCTCCTGAAGTTAGAGGATCTACTACTGTT  390
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331  GAAGTTAAGCCTAAAATCAGAGAAGAGGAGGCTCTCCTGAAGTTAGAGGATCTACTACTGTT  390

Qy     361  GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGACAAAGAAGGGGAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGACAAAGAAGGGGAT  420

Qy     391  GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGACAAAGAAGGGGAT  450
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391  GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGACAAAGAAGGGGAT  450

Qy     421  GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGCCCGCCCTGGCCCGGTGTCCCCAGCCTTCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGCCCGCCCTGGCCCGGTGTCCCCAGCCTTCC  540

Qy     451  GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGCCCGCCCTGGCCCGGTGTCCCCAGCCTTC  510
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451  GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCGCCCGCCCTGGCCCGGTGTCCCCAGCCTTC  510

Qy     481  GCGGGCCGCCTTCCAGTCCCCGGTGGATAATCCGCGCCCGCCCCACCTCGGCGCCCTTCCCCCGCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  GCGGGCCGCCTTCCAGTCCCCGGTGGATAATCCGCGCCCGCCCCACCTCGGCGCCCTTCCCCCGCC  540

Qy     511  GCGGGCCGCCTTCCAGTCCCCGGTGGATAATCCGCGCCCGCCCCACCTCGGCGCCCTTCGCCCGCC  570
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511  GCGGGCCGCCTTCCAGTCCCCGGTGGATAATCCGCGCCCGCCCCACCTCGGCGCCCTTCGCCCGCC  570

Qy     541  CTGCGCCCCCTGGAACTCCCGGTTCCAGCTCCCGAGAACTGCGCCTGCGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  CTGCGCCCCCTGGAACTCCCGGTTCCAGCTCCCGAGAACTGCGCCTGCGC  600

Qy     571  CTGCGCCCCCTGGAACTCCCGGTTCCAGCTCCCGAGAACTGCGCCTGCGC  630
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571  CTGCGCCCCCTGGAACTCCCGGTTCCAGCTCCCGAGAACTGCGCCTGCGC  630

Qy     601  AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGCGCTCCCGGTCCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGCGCTCCCGGTCCC  660

Qy     631  AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGCGCTCCCGGTCCC  690
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631  AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGCGCTCCCGGTCCC  690

Qy     661  GGGCGGGGGAGTACCGGGGCTCTTCGCAGCGTCATCGCAGCGGGGGCGTCGGGTCGCTTCCCGGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  GGGCGGGGGAGTACCGGGGCTCTTCGCAGCGTCATCGCAGCGGGGGCGTCGGGTCGCTTCCCGGC  720

Qy     691  GGGCGGGGGAGTACCGGGGCTCTTCGCAGCGTCATCGCAGCGGGGGCGTCGGGTCGCTTCCCGGC  750
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691  GGGCGGGGGAGTACCGGGGCTCTTCGCAGCGTCATCGCAGCGGGGGCGTCGGGTCGCTTCCCGGC  750

Qy     721  TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  780

Qy     751  TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  810
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751  TCGGAGCACACTGTGGAAGGCCACCGTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC  810

Qy     781  ACCGGCGCTTTTGCCAGAGTTGACGAGCGGCCCTGGGGCGTCGGGGCCGGGCCGGTGGTTGGGCC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811  ACCGGCGCTTTTGCCAGAGTTGACGAGCGGCCCTGGGGCGTCGGGGCCGGGCCGGTGGTTGGGCC  870

Qy     841  GCCTTTCTGGAGGAGGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871  GCCTTTCTGGAGGAGGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG  930

Qy     901  GAAGAAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGGACTGGACAGTATCTCCACTC  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931  GAAGAAAATCGCTGAGGAAGGCTCAGGAGACTCAGGTCCCAGGGACTGGACATATCTCGGCACTC  990

Qy     961  CTGCCCTCTGACTTCAGCCGCCTACTTCCAATATGAGGGGGTCTCTGAACTTCTGAACAGCTC  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     991  CTGCCCTCTGACTTCAGCCGCCTACTTCCAATATGAGGGGGTCTCTGAACTTCTGAACAGCTC  1050

Qy    1021  GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGCAGTGGATGCTGAGTGCTAAGCAGCTC  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051  GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGGATGATGCTGAGTGCTAAGCAGCTC  1110

Qy    1081  CACACCCTCTCTGACACCCCTGTGGGGGACCTGGGTGACTCTCGGGCTACAGCTGAACTTCCGA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1111  CACACCCTCTCTGACACCCCTGTGGGGGACCTGGGTGACTCTCGGGCTACAGCTGAACTTCCGA  1170

Qy    1141  GCGACGCAGCGCCTTTGAAATGGGCGAGTGATTGAATGAGGCCTCCTTCCCCTGCTGCTTGGACAGC  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1171  GCGACGCAGCGCCTTTGAAATGGGCGAGTGATTGAATGAGGCCTCCTTCCCCTGCTGCTTGGACAGC  1230

Qy    1201  AGTCCTCGGGCTGCTGAGCCAGTCAGCTGAATTCCTGCCTGGTCTGGCTGCTGGTGACATCCTA  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1231  AGTCCTCGGGCTGCTGAGCCAGTCAGCTGAAATTCCTGCCTGGTCTGGCTGCTGGTGACATCCTA  1290

Qy    1261  GCCCTGGTTTTGGCCTCCTTTTTCGCTGTCACCAGCGTGCGTTGCGTTCCTGCTTGGTTGCAGATGAGA  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1291  GCCCTGGTTTTGGCCTCCTTTTTCGCTGTCACCAGCGTCGCGTTCCTGCTTGGTCAGATGAGA  1350

Qy    1321  AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGACTACCGCCCAGCAGCAGAGGGTAGCCGAG  1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1351  AGGCAGCACAGAAGGGGGGAACCAAAGGGGGTGACTACCGCCCAGCAGCAGAGGGTAGCCGAG  1410

Qy    1381  ACTGGAGCCCTAGAGGCCTGGACTTCGTGGAGAATGTGAGAAGCCAGCCAGCAGGGCATCTGAGGG  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411  ACTGGAGCCCTAGAGGCCTGGACTTCGTGGAGAATGTGAGAAGCCAGCCAGCAGGGCATCTGAGGG  1470

Qy    1441  GGAGCCCGGTAACTGTCCTCTCCTCATTATGCCACTCCCTTTTTAAACTGCCAAGAAAATT  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1471  GGAGCCCGGTAACTGTCCTCTGCTCACTTCCTTTTTAAACTGCCAAGAAAATT  1530

Qy    1501  TTTTAAAATAAATATTTATAT  1522
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Db    1531  TTTTAAAATAAATATTTATAT  1552
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080

Query Match      100.0%;   Score 1522;   DB 10;   Length 1552;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 1522;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Qy      1  ACAGTCAGCCGCATGGCTCCCTGCCCTGCCCTGGCCTCCCTCTGTTGATCCCGGCC    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31  ACAGTCAGCCGCATGGCTCCCTGCCCTGCCCTGGCCTCCCTCTGTTGATCCCGGCC    90

Qy     61  CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCTCTGCACTGTCGATGCCTGTCCAT   120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91  CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCTCTGCACTGTCGATGCCTGTCCAT   150

Qy    121  CCCCAGAGGTTGCCCCGATGCAGGAGGAGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA   180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151  CCCCAGAGGTTGCCCCGATGCAGGAGGAGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA   210

Qy    181  GATGAACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGAATTCACCCAGAGGAGGAT   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211  GATGAACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGAATTCACCCAGAGGAGGAT   270

Qy    241  CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTGAGAGAGGAGGATCTACCT   300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271  CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTGAGAGAGGAGGATCTACCT   330

Qy    301  GAAGTTAAGCCTAAATCAGAAGAGAAGAGGGCTCCCTGAAGTTAGGAGTTACCTACTTGTT   360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331  GAAGTTAAGCCTAAATCAGAAGAGAAGAGGGCTCCCTGAAGTTAGGAGTTACCTACTTGTT   390

Qy    361  GAGGCTCCTTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAGAAGAGGGAT   420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391  GAGGCTCCTTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGACAAAGAAGAGGGAT   450

Qy    421  GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCCGGGGGTGTCCCCAGCCTGC   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451  GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCCGGGGGTGTCCCCAGCCTGC   510

Qy    481  GCGGGGCCGCTTCAGTTCCCGGGATATCCGCCCGCCCTTCTGCCCCCGCC   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511  GCGGGGCCGCTTCAGTTCCCGGGATATCCGCCCGCCCTTCTGCCCCCGCC   570

Qy    541  CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTTCCAGCTCCCAGAACTGCGCCCTGGCC   600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571  CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTTCCAGCTCCCAGAACTGCGCCCTGGCC   630

Qy    601  AACAATGGCCACAGTGTGCAACTAACCCTGCCTCCTGGGCTACGAGATGGCTCTGGGGTCCC   660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631  AACAATGGCCACAGTGTGCAACTAACCCTGCCTCCTGGGCTACGAGATGGCTCTGGGGTCCC   690

Qy    661  GGGCGGGGAGTACCGGGCGTCTGCAGCTCGCATCGTCGCAGGTGCTGGTCCCGGGC   720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691  GGGCGGGGAGTACCGGGCGTCTGCAGCTCGCATCGTCGCAGGTGCTGGTCCCGGGC   750

Qy    721  TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCTCAGC   780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751  TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACCTCAGC   810

Qy    781  ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCCTGGCCGGAGGCCTTGCTCGGCC   840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811  ACCGCCCTTTGCCAGAGTTGACGAGGCCTTGGGCGCCTGGCCGGAGGCCTTGCTCGGCC   870

Qy    841  GCCTTTCTTGGGAGGAGGGCCCGGAGAAAACAGTGCCTATGACGAGTTGCTGTCTCGCTG   900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871  GCCTTTCTTGGGAGGAGGGCCCGGAGAAAACAGTGCCTATGACGAGTTGCTGTCTCGCTG   930

Qy    901  GAAGAAATCGCTTGAGGAAGGCTCAGGAGACTCAGGTCCAGGGACACTATCTGCACTC   960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931  GAAGAAATCGCTTGAGGAAGGCTCAGGAGACTCAGGTCCAGGGACACTATCTGCACTC   990

Qy    961  CTGCCCTCTGACTTCAGCCGACTTCCAAATATGAGAGGGGGTCTCTGGAGGTGTGAGTGTCGATGCTGAGTGCTAAGCAGCTC   1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991  CTGCCCTCTGACTTCAGCCGACTTCCAAATATGAGAGGGGGTCTCTGGAGGTGTGAGTGTCGATGCTGAGTGCTAAGCAGCTC   1050

Qy   1021  GCCCAGGGTGTCATCTGACTGTGTTAAACCAGACACAGTCATGGGCTCTCGGAGTGGGACAGC   1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051  GCCCAGGGTGTCATCTGACTGTGTTAAACCAGACACAGTCATGGGCTCTCGGAGTGGGACAGC   1110

Qy   1081  CACACCCTCTCTGACACCCCTGTGGGGACCTGGGACTCGGACTTACAGCTGACTTCCGA   1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111  CACACCCTCTCTGACACCCCTGTGGGGACCTGGGACTCGGACTTACAGCTGACTTCCGA   1170

Qy   1141  GCGACGCAGCCTTTGAATGGGCCGAGTGATTGAGGCGCCTCCTTCCCTGCTGGGACAGC   1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171  GCGACGCAGCCTTTGAATGGGCCGAGTGATTGAGGCGCCTCCTTCCCTGCTGGGACAGC   1230

Qy   1201  AGTCCTCCGGGCTCCTCTGACCCAGCTGAGATTCCTCGCTGAGGCCAGTCCTGCTGAGCAGTCGGCATCCTA   1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231  AGTCCTCCGGGCTCCTCTGACCCAGCTGAGATTCCTCGCTGAGGCCAGTCCTGCTGAGCAGTCGGCATCCTA   1290

Qy   1261  GCCCTGGTTTTTGGGCCTCCTTTTGCTGTCACCGGCGTCGGGTTCCTTGCTGCTGGCTGCCTGGTGGTGACATCTTA   1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291  GCCCTGGTTTTTGGGCCTCCTTTTGCTGTCACCGGCGTCGGGTTCCTTGCTGCTGGCTGCCTGGTGGTGACATCTTA   1350

Qy   1321  AGGCAGCACGAGAGGGGAACCAAAGGGGGTGTGAGCGTACCGCCCAGCAGGATTAGCCAG   1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351  AGGCAGCACGAGAGGGGAACCAAAGGGGGTGTGAGCGTACCGCCCAGCAGGATTAGCCAG   1410

Qy   1381  ACTGGAGCCTAGAGGCTGGATCTTGGAGAGTGTGAGAGCCATCTGAGGG   1440
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1411  ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAGCCATCTGAGGG   1470

Qy   1441  GGAGCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT   1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1471  GGAGCCGGTAACTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT   1530

Qy   1501  TTTTAAAATAATATTTTATAAT   1522
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Db   1531  TTTTAAAATAATATTTTATAAT   1552
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RESULT 8
US-09-873-367C-516
; Sequence 516, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets.
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US20030165839A1
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 516
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-516

Query Match   100.0%;   Score 1522;   DB 10;   Length 1552;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCTCCCCTTCTGTTGGATCCCGGCC 60
Db     31 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCTCCCCTTCTGTTGGATCCCGGCC 90

Qy     61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGTCTCTCACTGTGTCTTCTGATGCTGTCCAT 120
Db     91 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGTCACTGTGTCTTCTGATGCTGTCCAT 150

Qy    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGGTCTTCTGGGGAA 180
Db    151 CCCCAGGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGGTCTTCTGGGGAA 210

Qy    181 GATGACCCACTGGGCGGCGAGGAGGATCGCCCAGTGAAGAGGATCTTCTGGGGAA 240
Db    211 GATGACCCACTGGGCGGCGAGGAGGATCTGCCCAGTGAAGAGGATCTTCTGGGGAA 270

Qy    241 CCACCCGGAGGAGGAGATCTACCTGGAGGAGGATCTACCT 300
Db    271 CCACCCGGAGGAGGAGATCTACCTGGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAATCAGAGAAGAAGAGGGCCTCCCTGAAGTTAGGAGGATCTACCTACTGTT 360
Db    331 GAAGTTAAGCCTAAATCAGAGAAGAAGAGGGCCTCCCTGAAGTTAGGAGGATCTACCTACTGTT 390

Qy    361 GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
Db    391 GAGGCTCCTGGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy    421 GACCAGAGTCATTGGGCGTATGGAGGGGACACGCCCGGGTGTCCCCAGCCTGC 480
Db    451 GACCAGAGTCATTGGGCGTATGGAGGGGACACGCCCGGGTGTCCCCAGCCTGC 510

Qy    481 GCGGGCCCTTCCAGTCCCGGTGGATATCCGCGCCCCAGCTGCCTTCTCGCCCGGCC 540
Db    511 GCGGGCCCTTCCAGTCCCGGTGGATATCCGCGCCCCAGCTGCCTTCTCGCCCGGCC 570

Qy    541 CTGCGCCCCCTGGGAACTCCTGGGCTTCCAGCTCCCAGAACTGCGCCTGCGCC 600
Db    571 CTGCGCCCCCTGGGAACTCCTGGGCTTCCAGCTCCCAGAACTGCGCCTGCGCC 630

Qy    601 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTGGCTAGAGATGGCTCTGGGGTCCC 660
Db    631 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTGGCTAGAGATGGCTCTGGGGTCCC 690

Qy    661 GGGGCGGGAGTACCGGGGCTTCTGCAGCTGCAGGTCGTTCCGGGC 720
Db    691 GGGGCGGGAGTACCGGGGCTTCTGCAGCTGCAGGTCGTTCCGGGC 750

Qy    721 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
Db    751 TCGGAGCACACTGTGGAAGGCCACCGGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 810

Qy    781 ACCGGCCTTGCCAGAGTTGACGAGGCCCTTGGCCGGCC 840
Db    811 ACCGGCCTTGCCAGAGTTGACGAGGCCCTTGGCCGGCC 870

Qy    841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTTG 900
Db    871 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTTG 930

Qy    901 GAAGAAATCGCTGAGGAAGGGCTCAGGACTCAGGTCCCAGGACATATCTGCACTC 960
Db    931 GAAGAAATCGCTGAGGAAGGGCTCAGGACTCAGGTCCCAGGACATATCTGCACTC 990

Qy    961 CTGCCCTCTTGACTTCAGCGCGCTACTTCCAAATATCAGGGGTCTCTGACTACACCCCTGT 1020
Db    991 CTGCCCTCTTGACTTCAGCGCGCTACTTCCAAATATCAGGGGTCTCTGACTACACCCCTGT 1050
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(second panel)

RESULT 9
US-09-968-007A-213

; Sequence 213, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 213
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-213

Query Match   100.0%;   Score 1522;   DB 11;   Length 1552;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 ACAGTCAGCGCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCTCCCCTTCTGTTGGATCCCGGCC 60
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(alignment rows in right panel)

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Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAGAGCTGAGTGATGAGTGCTCTGAGCTGAGTGCTGCTAAGCAGCTC 1080
Db   1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGAGAGCTGAGTGATGAGTGCTCTGAGCTGAGTGCTGCTAAGCAGCTC 1110

Qy   1081 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGTGTTAACCAGAGACAGTGAGCTGATGCTCCGA 1140
Db   1111 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGTGTTAACCAGAGACAGTGAGCTGATGCTCCGA 1170

Qy   1141 GCGAGCGCAGGCCTTTGAAATGGGGCGGAGTGATTGAGGGGCCTCCCTCCCTGCGCTAGCTGAGCAGC 1200
Db   1171 GCGAGCGCAGGCCTTTGAAATGGGGCGGAGTGATTGAGGGGCCTCCCTCCCTGCGCTAGCTGAGCAGC 1230

Qy   1201 AGTCCTCCGGGCTGTGAGCCGCCAGTCCAGCGTGACATCCTA 1260
Db   1231 AGTCCTCCGGGCTGTGAGCCGCCAGTCCAGCGTGACATCCTA 1290

Qy   1261 GCCCTGGGTTTTTTGGCCTCCTTTTGCTCGTCACGGGTCGCGGGTTCCTTGCTGCTGGTGACA 1320
Db   1291 GCCCTGGGTTTTTTGGCCTCCTTTTGCTCGTCACGGGTCGCGGGTTCCTTGCTGCTGGTGACA 1350

Qy   1321 AGGCAGCACAGAAGGGGAACCAAAAGGGGGGTGTGAGCTACCGCCAGCGTGGGAGTAGCCGAG 1380
Db   1351 AGGCAGCACAGAAGGGGAACCAAAAGGGGGGTGTGAGCTACCGCCAGCGTGGGAGTAGCCGAG 1410

Qy   1381 ACTGGAGCCTTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCGGCAGGATCTGAGGG 1440
Db   1411 ACTGGAGCCTTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCGGCAGGATCTGAGGG 1470

Qy   1441 GGAGCCGGGTAACTGTCCGTTCCGTTCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
Db   1471 GGAGCCGGGTAACTGTCCGTTCCGTTCCTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1530

Qy   1501 TTTTAAAATAAATATTTATTAAT 1522
Db   1531 TTTTAAAATAAATATTTATTAAT 1552
```

```
Db    1111  CACACCCTCTCGACACCCCTGGGGACGGACCTGGTGACTCTCGGCGTTGACTTCCGA  1170
Qy    1141  GCGACGCAGCCGCCTTTTGAATGGGCGAGTGAATTGAGGGCCTTCCTTCCCTGCTTGGGAGGTTGGACAGC  1200
Db    1171  GCCACGCAGCCCTTTGAATGGGCGGCCAGAGTGATTGAGGGCCTCCTTCCCTGCTTGGGAGGTTGGACAGC  1230
Qy    1201  AGTCCTCGGGCGTCGCTGAGCCAGTCCAGCTGGAATTCCTGCCTGGTGGTGACATCCTA  1260
Db    1231  AGTCCTCGGGCGTCGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGTGGTGACATCCTA  1290
Qy    1261  GCCCTGGTGTTTTGCCTTCCTTTTTGCTGTCACCAGGTCGTCGGTTGTTCTTGCAGATGAGA  1320
Db    1291  GCCCTGGTTTTTGGCCTCCTCTTTTGCGTGTCACCAGGTCGTCGTTGTTCCTTGTGCAGAGATGAGA  1350
Qy    1321  AGGCAGCACAGAAGGGGAACCAAAAGGGGTGTAGCTACCGGCCCAGCAGAGGGTAGCCCAG  1380
Db    1351  AGGCAGCACAGAAGGGGAACCAAAAGGGGTGTAGCTACCGGCCCAGCAGAGGGTAGCCCGAG  1410
Qy    1381  ACTGGAGCCTAGAGGGCTGGAGTCTTGAGAAGTGAGAAGCCAGCCAGCAGGGCCATCTGAGGG  1440
Db    1411  ACTGGAGCCTAGAGGGCTGGAGTCTTGAGGAAGTGAGAAGCCAGCCAGCAGGGCCATCTGAGGG  1470
Qy    1441  GGAGCCGGTAACTGTCCTGTCCTGTCCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT  1500
Db    1471  GGAGCCGGTAACTGTCCTGTCCTGTCCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT  1530
Qy    1501  TTTTAAAATAAATTAATTATTTATAAT  1522
Db    1531  TTTTAAAATAAATTAATTATTTATAAT  1552
```

RESULT 10
US-10-301-822-11

; Sequence 11, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPN01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)...(1422)
US-10-301-822-11

Query Match   100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1  ACAGTCAGCCGCATGGCTCCCCGTGGGACCTGGTGACTCTCGGCGTTGACTTCCGA  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 11
US-10-465-572-9
; Sequence 9, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-465-572-9

Query Match   100.0%;   Score 1522;   DB 15;   Length 1552;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy      1 ACAGTCAGCCGCATGGGCTCCCCGTGCCCCAGCCCCGCCCTCCTCTGTTGATCCCGGCC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     31 ACAGTCAGCCGCATGGGCTCCCCGTGCCCCAGCCCCGCCCTCCTCTGTTGATCCCGGCC   90

Qy     61 CCTGCTCCAGGCCTCACTGTGCCAACTGCTGCTGCTCGTTCTGATGCCTGTCCAT     120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGCCTCACTGTGCCAACTGCTGCTGCTCGTTCTGATGCCTGTCCAT     150
```

RESULT 12
US-10-172-118-574
; Sequence 574, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

Query Match   100.0%;   Score 1522;   DB 15;   Length 1552;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1522;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

```
Qy    241 CCACCCGGAGGAGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGGATCTACCT 300
Db    271 CCACCCGGAGGAGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGATCTACCTACTT 330

Qy    301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 360
Db    331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTGTT 390

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGACAAAAGGGGAT 420
Db    391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAAATAATGCCCACAGGGACAAAAGGGGAT 450

Qy    421 GACCAGAGTCATTGGGCGTATTGGGAGGCGACCCCGCGCCCCGGGTGTCCCAGCCTGC 480
Db    451 GACCAGACTCATTGGGCGTATGGAGGCGACCCCGCGCCCCGGGTGTCCCAGCCTGC 510

Qy    481 GCGGGGCCGCTTTCCAGTCCCCGGTGGATATCCGGCCCCCAGCTCGCCGCCTTCTGCCCGC 540
Db    511 GCGGGGCCGCTTTCCAGTCCCCGGTGGATATCCGGCCCCCCAGCTCGCCGCCTTCTGCCCGC 570

Qy    541 CTGCGCCCCCTGAACTCCCTGGGCTTCAGCTCCCCAGAACTGGGCCTTGCGC 600
Db    571 CTGCGCCCCCTGAACTCCCTGGGCTTCAGCTCCCCAGAACTGGGCCTTGCGC 630

Qy    601 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTTCCTGGGCTTCGGGGTCCC 660
Db    631 AACAAATGGCCACAGTGTGCAACTGACCCTGCCTTCCTGGGCTTCGGGGTCCC 690

Qy    661 GGGCGGGAGTACCGGGCTCTCGCAGCTGCATCTGGGGGGCTGCAGGGTCGGTCGTCCGGGGC 720
Db    691 GGGCGGGAGTACCGGGCTCTCGCAGCTGCATCTGGGGGGCTGCAGGGTCGGTCGTCCGGGGC 750

Qy    721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
Db    751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 810

Qy    781 ACCGGCCCTTTGCCAGAGTTGACAGAGGCCTTGGGCCGTTGGGCCGTGTTGGCC 840
Db    811 ACCGGCCTTTGCCAGAGTTGACAGAGGCCTTGGGCCGTTGGGCCGTGTTGGCC 870

Qy    841 GCCTTTCTGGAGGAGGGGCCGGAGAAGAAAACAGTGCCCTTATGAGCAGTTGCTGTCTTG 900
Db    871 GCCTTTCTGGAGGAGGGGCCGGAGAAGAAAACAGTGCCCTTATGAGCAGTTGCTGTCTTG 930

Qy    901 GAAGAAATCGCTGAGGAAGGCTCAGGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
Db    931 GAAGAAATCGCTGAGGAAGGCTCAGGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990

Qy    961 CTGGCCCTCTGACTTCAGCGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACGCCCTGT 1020
Db    991 CTGCCCCTCTGACTTCAGCGCGCTACTTCCAAATATGAGGGGTCTCTGACTACACGCCCTGT 1050

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTTGTTTAACCAGACAGTGATGCTGAGTGCTGCTCAGCAGCTC 1080
Db   1051 GCCCAGGGGTGTCATCTGGACTGTTGTTTAACCAGACAGTGATGCTGAGTGCTGCTCAGCAGCTC 1110

Qy   1081 CACACCCTCTCTGACACCCTGGTTGGTTGACTCTGGGGCTACTGAACTTCCGA 1140
Db   1111 CACACCCTCTCTGACACCCTGGTTGGTTGACTCTGGGGCTACTGAACTTCCGA 1170

Qy   1141 GCGGACGGCAGCCTTTGAATGGGCGGAGTCGATTGAGGGCCTCCTTCCCTGGCTACTGGT 1200
Db   1171 GGGACGCAGCCTTTGAATGGGCGGAGTCGATTGAGGGCCTCCTTCCCTGGCTACTGGT 1230

Qy   1201 AGTCCTCGGCGCTGAGCCGAGTGAATTCCTGCTCCTCGCGCTCCGCTCGC 1260
Db   1231 AGTCCTCGGCGCTGAGCCAGTGAATTCCTGCTCCTCGCGCTCCGCTCGC 1290

Qy   1261 GCCCTGGTTTTGGCCTCCTTTGGCTCTGTCACCAGCGGTCGGCGTTCCTGCTGGTGACATCCTA 1320
Db   1291 GCCCTGGTTTTGGCCTCCTTTGGCTCTGTCACCAGCGGTCGGCGTTCCTGCTGGTGACATCCTA 1350

Qy   1321 AGGCAGCACGAGAGGGGAACCAAAGGGGGGTGTGAGCTACCGCCCCAGCAGAGGTTAGCCCGAG 1380
Db   1351 AGGCAGCACGAGAGGGGAACCAAAGGGGGGTGTGAGCTACCGCCCCAGCAGAGGTTAGCCCGAG 1410

Db   1411 ACTGGAGCCTAGAGGCTGGACATCTTGGAGAATGTGAGAAGCCAGCTCATCTGAGGG 1470
Db   1471 GGAGCCGGGTAACTGTCCCTGCCTCATTATCGCCACTTCCTTTAACTGCCAAGAAATT 1530
Db   1531 TTTTAAATAAAATATTTTATAAT 1552
```

```
Qy          361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy          421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510

Qy          481 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          511 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 570

Qy          541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          571 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCGC 630

Qy          601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          631 AACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 690

Qy          661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          691 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGGC 750

Qy          721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAGC 810

Qy          781 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          811 ACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGCC 870

Qy          841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          871 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930

Qy          901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990

Qy          961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050

Qy         1021 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1051 GCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1110

Qy         1081 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1111 CACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA 1170

Qy         1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1171 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1230

Qy         1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1290

Qy         1261 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1291 GCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1350

Qy         1321 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1351 AGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1410

Qy         1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1470

Qy         1441 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1471 GGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT 1530

Qy         1501 TTTTAAAATAAATATTTATAAT 1522
                ||||||||||||||||||||||
Db         1531 TTTTAAAATAAATATTTATAAT 1552

RESULT 13
US-10-388-360-291
; Sequence 291, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
;  APPLICANT: GENOMIC HEALTH
;  APPLICANT:  Baker, Joffre B.
;  APPLICANT:  Cronin, Maureen T.
;  APPLICANT:  Kiefer, Michael C.
;  APPLICANT:  Shak, Steve
;  APPLICANT:  Walker, Michael Graham
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
;  FILE REFERENCE: 39740-0001US
;  CURRENT APPLICATION NUMBER: US/10/388,360
;  CURRENT FILING DATE:  2003-03-12
;  PRIOR APPLICATION NUMBER: US 60/412,049
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: US 60/364,890
;  PRIOR FILING DATE: 2002-03-13
;  NUMBER OF SEQ ID NOS: 384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 291
;   LENGTH: 1552
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-388-360-291

  Query Match             100.0%;  Score 1522;  DB 15;  Length 1552;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1522;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           31 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC 90

Qy           61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 150

Qy          121 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          151 CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 210

Qy          181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          211 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 270

Qy          241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy          301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy          361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy          421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510

Qy          481 GCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCCAGCTCGCCGCCTTCTGCCCGGCC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 14
US-10-295-027-305

```
Db  511 GCGGGCCGGGCCGCTTCCCAGTCCCCGGTGGATATCCGCGCCCCCAGCTCGGCCGCCTTCTGCCCCGGCC
Qy  541 CTGGCGCCCCCCCCTGGAACTCCTCGGGCTTCCAGTTCCCAGTTCCCAGGAACTGCGCGCCCTGGCGC
Db  571 CTGCGCCCCCCCCTGGAACTCCTCGGGCTTCCAGTCCCAGGAACTGCGCGCCCTGGCGC
                                                                          630
Qy  601 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  631 AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGGTCCC
                                                                          690
Qy  661 GGGGCGGGAGTACCCGGGCTTCTGCAGCTGCATCTGTCGCACTGGGGGGCTTGCAGGTGGTCGTCCCGGGC
Db  691 GGGGCGGGAGTACCCGGGCTTCTGCAGCTGCATCTGTCGCACTGGGGGGCTTGCAGGTGGTCGTCCCGGGC
                                                                          750
Qy  721 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCAGGATCCACGTGGTTCACCTCAGC
Db  751 TCGGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCCAGGATCCACGTGGTTCACCTCAGC
                                                                          810
Qy  781 ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGGCGCCCGGGAGGCCTGGGCCGTGGTGTTGGGCC
Db  811 ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGGCGCCCGGGAGGCCTGGGCCGTGGTGTTGGGCC
                                                                          870
Qy  841 GCCTTTTCTTGGAGGAGGAGGGGCCCGGAGAAGAGAAAAACAGTTGCCTTATGCAGTTGTCGTCTCGCTTG
Db  871 GCCTTTTCTTGGAGGAGGAGGGGCCCGGAGAAGAGAAAAACAGTTGCCTTATGCAGTTGTCGTCTCGCTTG
                                                                          930
Qy  901 GAAGAAATCGCTGAGGAAGGCTTCAGAGACTCAGGTCCCAGGACTCGGACATATCTGCACTC
Db  931 GAAGAAATCGCTGAGGAAGGCTTCAGAGACTCAGGTCCCAGGACTCGGACATATCTGCACTC
                                                                          990
Qy  961 CTGCCCTTGACTTCAGCCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACCGCCCCTGT
Db  991 CTGCCCTTGACTTCAGCCGCTACTTCCAAATATGAGGGGGTCTCTGACTACACCGCCCCTGT
                                                                          1050
Qy 1021 GCCCAGGGGTGTCATCTGACTCGTGTTTTAAACCAGACAGTGATCCTGACTGTGCTAAGCACTC
Db 1051 GCCCAGGGGTGTCATCTGACTCGTGTTTTAAACCAGACAGTGATCCTGACTGTGCTAAGCACTC
                                                                          1110
Qy 1081 CACACCCCTCTCTGACACACCCTGTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA
Db 1111 CACACCCCTCTCTGACACACCCTGTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGA
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Qy 1141 GCGACGCAGCCTTGAATGGGCGGAGTGAATTCTCGGCTCCTTCCCGTCCCGGGGACAGC
Db 1171 GGGACGCAGCCTTTGAATGGGCGGAGTGAATTCTCGGCTCCTTCCCGTCCCGGGGACAGC
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Qy 1201 AGTCCTCCGGGCTGCCTGAGCCAGTCCAGCTGAATTCTTCTCGGCCTCTGCCTGCTGCGCTGGTGGACAATCCTA
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Qy 1261 GCCCTCGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGGTCGCGGTTCCTTGGTTGCAGATGAGA
Db 1291 GCCCTCGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGGTCGCGGTTCCTTGGTTGCAGATGAGA
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Db 1351 AGGCAGCACAGAAGGGGAACCAAGGGGGGTGTGAGCTACCGGCCACGAGAGGTAGCCGAG
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Qy 1381 ACTGGAGCCTAGAGGCTAGCTTGGGACAAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG
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Db 1471 GGAGCCCGTAACTGTCTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAAATT
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Qy 1501 TTTTAAAATAAATATATTTATAAT
Db 1531 TTTTAAAATAAATATATTTATAAT 1552
            1522
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Query Match         100.0%;  Score 1522;  DB 15;  Length 1552;
Best Local Similarity 100.0%;  Pred. No. 0;  Mismatches 0;
Matches 1522;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 ACAGTCAGCCGCATNGGCTTCCCCCTGTGCCCCAGCCCTGGCTCCCTCCCTCGTTGATCCCGCGCC
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Qy  61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTGTCACTGCTCCTTTCTGATGCTGTCCAT
Db  91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTGTCACTGCTCCTTTCTGATGCTGTCCAT
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Qy 121 CCCCAGGAGGTTGCCCCCGGATGCAGGACGAGAATTCCCCCCTTGGGGAGGAGGCTTCTTCTTGGGGAA
Db 151 CCCCAGGAGGTTGCCCCCGGATGCAGGACGAGAATTCCCCCCTTGGGGAGGAGGCTTCTTCTTGGGGAA
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Qy 181 GATGACCCACTCGGGCGGAGGAATCTGCCCAGTGAAGAGGAGGAGTTCACCGAGGAGGAT
Db 211 GATGACCCACTCGGGCGGAGGAATCTGCCCAGTGAAGAGGAGGAGTTCACCGAGGAGGAT
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Qy 241 CCACCCCGAGGAGGATCTACCTGGAGGAGGATCTACCT
Db 271 CCACCCCGAGGAGGATCTACCTGGAGGAGGATCTACCT
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Qy 301 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGAGGATCTACCTACTNGTT
Db 331 GAAGTTAAGCCTAAATCAGAAGAAGAAGAGGGCTCCCTGAAGTTAGAGAGGATCTACCTACTNGTT
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Db    361 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
Qy    391 GAGGCTCCTGGAGGATCCTCAAGAACCCCAGAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450
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Qy    421 GACCAGAGTCATTGGCGCTATGGAGCCGACCCGGCCCTTATGGAGGGTGCCCAGCCTGC 480
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Qy    631 AACAATGGCCCACAGTGTGCAACTGACCCTGCCTCCCTGGGCTCAGAGAGGTGGCTCTGGGTCCC 690
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Qy    751 TCGGAGCACACTGTGGAGGCCACCGTTCCCTGCCAGGACATCCACGTGGTTCACCTCAGC 810
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RESULT 15
US-10-295-027-1022
; Sequence 1022, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-0125000US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1022
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1022

Query Match   100.0%; Score 1522; DB 15; Length 1552;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  1501 TTTTAAAATAAATTATTTTATAAT 1522
         |||||||||||||||||||||||
Db  1531 TTTTAAAATAAATTATTTTATAAT 1552
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Job time : 866 secs

OM nucleic - nucleic search, using sw model

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Run on: February 5, 2005, 23:51:49 ; Search time 4444 Seconds
                                            (without alignments)
                                            12480.034 Million cell updates/sec

Title: US-09-967-237A-1
Perfect score: 1522
Sequence: 1 acagtcagccgcatggctcc..........ttaaaataatatattataat 1522

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Databases :   EST:*
                1: gb_est1:*
                2: gb_est2:*
                3: gb_htc:*
                4: gb_est3:*
                5: gb_est4:*
                6: gb_est5:*
                7: gb_est6:*
                8: gb_est7:*
                9: gb_est2:*
                9: gb_gss:*
                9: gb_gss1:*
                9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1	c	1510.4	99.2	1541	3	CR597234	CR597234 full-leng
2		1502.4	98.7	1523	3	CR620502	CR620502 full-leng
3	c	1467.4	96.4	1469	3	CR616345	CR616345 full-leng
4	c	1423.4	93.5	1492	3	CR590646	CR590646 full-leng
5	c	1024.8	67.3	1084	1	AL542336	AL542336
6		920.8	60.5	1070	1	AL554705	AL554705
7	c	903.4	59.4	1009	1	AL558378	AL558378
8	c	891.4	58.6	916	5	BX423970	BX423970
9	c	861.6	56.6	1071	1	AL554665	AL554665
10	c	832	54.7	1017	1	AL554665	AL554665
11	c	813.6	53.5	961	5	BX401186	BX401186
12		797	52.4	971	7	BX423969	BX423969
13	c	794.4	52.2	994	7	CO579387	CO579387
14	c	789.4	51.9	1017	1	AL577748	AL577748
15	c	772.6	50.8	927	1	AL580216	AL580216
16	c	731.4	48.1	874	4	AL555184	AL555184
17	c	669.8	44.0	689	6	BG386425	BG386425
18	c	669.8	44.0	689	6	CA425935	CA425935 UI-H-FE1-
19	c	665.4	43.7	682	1	AI831707	AI831707 wj40h01.x
20	c	660.4	43.4	836	5	BX383092	BX383092
21	c	660.4	43.4	691	5	BU620600	BU620600 UI-H-FL1-
22	c	650.6	42.7	795	2	AW083555	AW083555 xc14g03.x
23		647	42.5	669	1	AI925646	AI925646 wo32d07.x
24	c	629.2	41.3	733	4	BG819731	BG819731

Result No.		Score	Query Match	Length	DB	ID	Description
25	c	627.8	41.2	658	1	AI769526	AI769526 wj24a11.x
26	c	625.6	41.1	818	2	BE548062	BE548062 601072095
27	c	620.8	40.8	806	2	BF344769	BF344769 602014025
28	c	608.4	40.0	659	6	CA416326	CA416326 UI-H-FE0-
29	c	586.4	38.5	589	8	BM790508	BM790508 K-EST0070
30	c	582.2	38.3	618	2	AW615291	AW615291 hh40f01.x
31	c	580	38.1	740	7	CK971835	CK971835 4088027 B
32	c	575.6	37.8	814	1	AI241681	AI241681 qu70e12.x
33	c	572	37.6	627	4	BM552941	BM552941 AGENCOURT
34	c	568.8	37.4	830	7	BI223232	BI223232 602941237
35	c	568.6	37.4	746	4	BM552941	BM552941 AGENCOURT
36	c	564	37.1	577	7	CK849799	CK849799 972939 BA
37	c	541.6	35.6	736	1	AI032380	AI032380 ov37e07.x
38	c	533.6	35.1	722	7	BE543633	BE543633 601071359
39	c	522.6	34.3	581	1	CK978804	CK978804 411017 B
40	c	520.6	34.2	581	1	AI023541	AI023541 ov79e12.x
41	c	514.6	33.8	543	1	AI023541	AI023541 ov79e12.x
42	c	512	33.6	579	1	CK969500	CK969500 4084712 B
43	c	501.2	33.0	525	1	AA879425	AA879425 oj191d02.s
44	c	495.8	32.6	551	6	AI400286	AI400286 tg43c07.x
44	c	501.8	33.0	579	1	AI979142	AI979142 wr71a08.x
44	c	489	32.1	551	6	CA063362	CA063362 1002511 H
45		489	32.1	489	1	AI791726	AI791726 oq68b07.y

ALIGNMENTS

RESULT 1
CR597234
LOCUS   CR597234   1541 bp   mRNA   linear   HTC 21-JUL-2004
DEFINITION   full-length cDNA clone CS0DI085YF18 of Placenta Cot 25-normalized
                of Homo sapiens (human).
ACCESSION   CR597234
VERSION   CR597234.1   GI:50478041
KEYWORDS   HTC; CNSLT_cDNA.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1   (bases 1 to 1541)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished
REMARK   Contact : Feng Liang Email : fliang@lifetech.com URL :
                http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
                Faraday Avenue
REFERENCE   2   (bases 1 to 1541)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                end enriched, double-strand cDNA was digested with Not I and cloned
                into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                was normalized. Library was constructed by Life Technologies, a
                division of Invitrogen.
FEATURES   Location/Qualifiers
   source   1..1541
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DI085YF18"
                /tissue_type="Placenta Cot 25-normalized"
                /plasmid="pCMVSPORT_6"
ORIGIN

Query Match   99.2%; Score 1510.4; DB 3; Length 1541;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1511; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 ACAGTCAGCCGCATGGCTCCCTCCCCTGTGCCCCAGCCCCTGGCTCTCCTTCTGTTGATCCCGGCC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 ACAGTCAGCCGCATGGCTCCCTCCCCTGTGCCCCAGCCCCTGGCTCTCCTTCTGTTGATCCCGGCC 89

```
Qy      61 CCTGCTTCCAGGCCCTCACTGTGCAAACTGCTGTCTGCTGCTTCTGATGCCTGTCCAT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 CCTGCTTCCAGGCCCTCACTGTGCAAACTGCTGTCTGCTGCTTCTCGTGCCTGTCCAT 149

Qy     121 CCCCAGAGAGGTTGCCCCGGATGCAGGAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGGAA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 CCCCAGAGAGTTGCCCCGGATGCAGGAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGGA 209

Qy     181 GATGACCCACTGGGCGACGGAGGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGGAGGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 GATGACCCACTGGGCGACGGAGGAGGATCTGCCCAGTGAAGAGGAGGATTCACCCAGAGGAGGAT 269

Qy     241 CCACCCGGAGAGGAGGGAGGATCTACCTTGGAGAGGAGGAGGATCTACCT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     270 CCACCCGGAGAGGAGGGAGGATCTACCTTGGAGAGGAGGAGGATCTACCT 329

Qy     301 GAAGTTAAGGCCTAAATCAGGAAGAAGAGGGCTCCCTGAAGTTAAGGATTACTTACCTTACTGTT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     330 GAAGTTAAGGCCTAAATCAGGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACACTACTGTT 389

Qy     361 GAGGCTCCTGGAGGATCCTCAAGAAGACCCCAGAAATAAATGCCCACAGAGGAGAAAGAAGAGGGAT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     390 GAGGCTCCTGGAGATCCTCAAGAAGACCCCAGAAATAATGCCCACAGAGGAGAAAGAAGAGGGGAT 449

Qy     421 GACCAGAGAGTCAATTGGGGCTATGGAGAGGCGGACCACCGCCCTGGCCCCTGGCCGTGTCCCCAGCCTGC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     450 GACCAGAGAGTCAATTGGGGCTATGGAGAGGCGGACCACCGCCCTGGCCCCTGGCCGTGTCCCCAGCCTGC 509

Qy     481 GCGGGCCGCGCTTCCAGTCCCCGGTGGATATTCCGCCCCCCAGCTCCTGGCCCCGGCCGCTGC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     510 GCGGGCCGCGCTTCCAGTCCCCGGTGGATATTCCGCCCCCCAGCTCCTGGCCCCGGCCGCC 569

Qy     541 CTGCGCGCCCCCCGGGAACTCCTGGGCGCTTCCAGCTCCCAGCTCCCGCGCCCTGGCC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     570 CTGCGCGCCCCCTGGGAACTCCTGGGCGCTTCCAGCTCCCAGCTCCCGCGCCCTGGCC 629

Qy     601 AACAATGGCCACAGTGTGCAACTGACCCTGCTCCTCTGGGCTAGAGATGGCTGGGTCCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     630 AACAATGGCCACAGTGTGCAACTGACCCTGCTCCTCTGGGCTAGAGATGGCTGGGTCCC 689

Qy     661 GGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTCACCTGGGGGCCTGCAGGTGCTGTCCGGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     690 GGGCGGGAGTACCGGGGCTCTGCAGCTGCATCTCACCTGGGGGCCTGCAGGTGCTGTCCGGC 749

Qy     721 TCGGGAGCACACTGTGTGGAAGGGCACCACCGTTTCCCTGCCGAGATCCAGATCCAGGTTCACCTCAGC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     750 TCGGAGCACACTGTGGAAGGGCACCACCGTTTCCCTGCCGAGATCCAGTTCACCTCAGC 809

Qy     781 ACCGGCCTTTGCCAGAGTTGACGAGGCGTTGGGGGCCTTGGGGCTGGGCCGTGTTGGCC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     810 ACCGGCCTTTGCCAGAGTTGACGAGGCGTTGGGGGCCTTGGGGCTGGGCCGTGTTGGCC 869

Qy     841 GCCTTTCTGGGAGGAGGGCCCGGAGAGAAAAACAGTGGCCTATGAGCGAGTGTGCTGTTCTCGCTTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 GCCTTTCTGGGAGGAGGGCCCGGAGAGAAAACAGTGGCCTATGAGCAGTTGCTGTTCTCGCTTG 929

Qy     901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 989

Qy     961 CTGCCCTTCTGACTTCAGCCGCTACTTCCAAATATGAGGGGTCTTCTGACTACACACCGCCCTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 CTGCCCTTCTGACTTCACCCGCTACTTCCAAATATGAGGGGTCTTCTGACTACACCGCCCTGT 1049

Qy    1021 GCCCAGGGGTGTCATCTGACTGTTTTAACCAGACAGTGATGCTGAGTGCTGAGTAGCAGCTC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 GCCCAGGGGTGTCATCTGACTGTGTTTAACCAGACAGTGATCTGAGTGCTGAGTAGCAGCTC 1109

Qy    1081 CACACCCTCTCTGACACCGTGGGGGACCTGGTGACTCTCGGCCTACACAGCTGAACTTCCGA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 CACACCCTCTCTGACACCCTGTGGGGGACCTGGTGACTCTCGGCCTACAGCTGAACTTCCGA 1169
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Qy    1141 GCGACGCAGCGCCTTTGAATGGGCGCAGTGATTGAGGGCCTCCTTCCCTGCTGGACAGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1170 GCGACGCAGCGCCTTTGAATGGGCGCAGTGAATTCCTGCCTGGCTGCTGGTGACACTCCTTA 1229

Qy    1201 AGTCCTTCGGGCTCCTGCTGAGCCGACGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 AGTCCTTCGGGCTGCTGAGCCGACGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA 1289

Qy    1261 GCCCTGGTTTTGGCCTTCCTTTTTTTGCTGTCACCAGCGCGTCGCGGTTCCTTGTTCTGCAGATGAGA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1290 GCCCTGGTTTTTGGCCTCCTTTTTTTGCTGTCACCAGCGCGTCGCGGTTCCTTGTTCTGCAGATGAGA 1349

Qy    1321 AGGCAGCACAGAGAAGGGGGGAACCAAAAGGGGGTGTGAGCTACCGCGCGCAGCAGAGGTAGCCGAG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1350 AGGCAGCACAGAGAAGGGGGAACCAAAAGGGGTGTGAGCTACCGCGCCCAGCAGAGGTAGCCGAG 1409

Qy    1381 ACTGGAGCCTAGAGGCTGGAGAAATGTGAGAAATGTGAGAGCTAGAGGCCAGCCCAGCCACTCTGAGGG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1410 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAGCCAGCCCAGCCATCTGAGGG 1469

Qy    1441 GGAGCCGGTAACTGTCCGTGTCCGTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1470 GGAGCCGGTAACTGTCCGTGTCCGTGCTCATTATGCCACTTCCTTTTTAACTGCCAAGAAATT 1529

Qy    1501 TTTTAAAATAAA 1512
           ||||||||||||
Db    1530 TTTTAAAATAAA 1541
```

RESULT 2
LOCUS   CR620502   1523 bp   mRNA   linear   HTC 21-JUL-2004
CR620502
DEFINITION full-length cDNA clone CS0DK007YK10 of Hela cells Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR620502
VERSION   CR620502.1 GI:50501309
KEYWORDS   HTC; CNSlT_cDNA.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1523)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK   Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2 (bases 1 to 1523)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..1523
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK007YK10"
                     /tissue_type="HeLa cells Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match   98.7%; Score 1502.4; DB 3; Length 1523;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1503; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy      1  ACAGTCAGCGCAATGGCTCCCCTGTCCCCTGCCC                                                   60
           |||||||||||||||||||||||||||||||||||
Db     20  ACAGTCAGCGCAATGGCTCCCCTGTCCCCTGCCC                                                   79

Qy     20  CCTGCTCCAGGGCTTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT                                    120
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     80  CCTGCTCCAGGGCTTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT                                    139

Qy     61  CCTGCTCCAGGGCTTCACTGTGCAACTGCTGCTTCTGATGCCTGTCCAT                                    120
Db    120                                                                                    139

Qy    121  CCCCAGAGGTTGCCCCGGAGTGCAGGAGGATTCCCCTGGGAGGAGGAA                                     180
Db    140  CCCCAGAGGTTGCCCCGGAGTGCAGGAGGATTCCCCTGGGAGGAGGAA                                     199

Qy    121  CCCCAGAGGTTGCCCCGGAGTGCAGGAGGATT                                                     180
Db    181  GATGACCCACTGGGCGGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT                             240

Qy    181  GATGACCCACTGGGCGGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGGAGGAT                             240
Db    200  CCACCCGGAGAGGAGGATCTACCTGGAGGAGGATCTACCT                                             259

Qy    241  CCACCCGGAGAGGAGGATCTACCTGGAGGAGGATCTACCT                                             300
Db    260  CCACCCGGAGAGGAGGATCTACCTGGAGGAGGATCTACCT                                             319

Qy    301  GAAGTTAAGCCTAAATCAGAGAGAAGAGGGCTCCCTGAAGTTAGAGGATTACCTACTGTT                          360
Db    320  GAAGTTAAGCCTAAATCAGAGAGAAGAGGGCTCCCTGAAGTTAGAGGATTACCTACTGTT                          379

Qy    361  GAGGCTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACACAGGGGA                                     420
Db    380  GAGGCTCCTGGAGATCCTCAAGAACCCAGAATAATGCCCACACAGGGGA                                     439

Qy    421  GACCAGGACTCATTGGGCGGCTATGGAGGCGGA                                                    480
Db    440  GACCAGAGTCATTGGGCGGCTATGGAGGCGGA                                                     499

Qy    481  CTGCGGCCCGGCTTCCAGTGCCCGGTGGATATCCGGCC                                               540
Db    500  GCGGCGGCCGGCTTCCAGTGCCCGGTGGATATCCGGCC                                               559

Qy    541  CTGCGGCCCCCTGGAACTCCTGGGGTTCAGCTCCCG                                                  600
Db    560  CTGCGGCCCCCTGGAACTCCTGGGGTTCAGCTCCCG                                                  619

Qy    601  AACAATGGCCACAGTGTGCAACTGACCCTGCC                                                     660
Db    620  AACAATGGCCACAGTGTGCAACTGACCCTGCC                                                     679

Qy    661  GGGCGGGGAGTACCCGGGCCTCTGCACTGCAC                                                     720
Db    680  GGGCGGGGAGTACCCGGGCCTCTGCACTGCAC                                                     739

Qy    721  TCGGAGCACACTGTGGAAGGGCCACACCGTTTCCCTGCC                                              780
Db    740  TCCGAGCACACTGTGGAAGGGCCACCGTTTCCCTGCC                                                799

Qy    781  ACGGCCTTTGCCAGAGTTGACGAGGCCTTGGCC                                                    840
Db    800  ACCGGCCTTTGCCAGAGTTGACGAGGCCTTGGCC                                                   859

Qy    841  GCCTTTCTCGGAGGAGGGCCCGGAAGAAAACAGTGCC                                                900
Db    860  GCCTTTCTCGGAGGAGGGCCCCGGAAGAAAACAGTGCC                                               919

Qy    901  GAAGAAAATCGCTGAGGAGGGCTCAGAGACTCAGGTTC                                               960
Db    920  GAAGAAAATCGCTGAGGAGGGCTCAGAGACTCAGGTTC                                               979

Qy    961  CTGCCCTCTTGACTTCAGCCGCTACTTCCAAATATGAGGG                                             1020
Db    980  CTGCCCTCTTGACTTCAGCCGCTACTTCCAAATATGAGGG                                             1039

Qy   1021  GGCCAGGGGTGTCATCTGGAC                                                                1080
Db   1040  GGCCCAGGGGTGTCATCTGGAC                                                               1099

Qy   1081  CACACCCTCTCTGACACCCTGTGGGACCTGGCTAC                                                  1140
Db   1100  CACACCCTCTCTGACACCCTGTGGGACCTGGCTAC                                                  1159

Db   1141  GCGACGCAGCCGTTTGAAATGGGCGGAGTGATTGAGCGCCT                                            1200

Db   1160  GCGACGCAGCCTTTGAAATGGGCGGAGTGATTGAGCAGC                                              1219

Db   1201  AGTCCTCGGCGCTGCTGAGCCAGTCCAGCTGAAATTCC                                               1260

Db   1220  AGTCCTCGGCGCTGCTGAGCCAGTCCAGCTGAAATTCCTA                                             1279

Db   1261  GCCCTGGTTTTGGCCTCCTTTTGTCGTCACCAGCGTCG                                               1320

Db   1280  GCCCTGGTTTTGGCCTCCTTTTGTCGTCACCAGCGTCG                                               1339

Db   1321  AGGCAGCACAGAAGAGGGGACCAAAGGGCGGTGT                                                   1380

Db   1340  AGGCAGCACAGAAGAGGGGACCAAAGGGCGGTGT                                                   1399

Db   1381  ACTCGGAGCCTAGCAGGCTGGATCGATCTTGGAGA                                                  1440

Db   1400  ACTCGGAGCCTAGCAGGCTGGATCGATCTTGGAGA                                                  1459

Db   1441  GGAGCCGGTAACTGTCCTGTCCTGCTGCTCATTA                                                   1500

Db   1460  GGAGCCGGTAACTGTCCTGTCCTGCTGCTCATTA                                                   1519

Qy   1501  TTTT                                                                                1504
           ||||
Db   1520  TTTT                                                                                1523
```

RESULT 3

```
LOCUS       CR616345                1469 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DA003YB12 of Neuroblastoma of Homo
            sapiens (human).
ACCESSION   CR616345
VERSION     CR616345.1  GI:50497152
KEYWORDS    HTC; CNSI_T_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1469)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1469)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..1469
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DA003YB12"
                     /tissue_type="Neuroblastoma"
                     /plasmid="pCMVSPORT_6"
ORIGIN
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Query Match 96.4%; Score 1467.4; DB 3; Length 1469;

Best Local Similarity 99.9%; Conservative 0; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 1468;

```
Qy     9 CCGCATGGCTCCCCGTGCCCCAGCCCCTTGGCTCCTGGCTCCCGTGCCCCCTGCCCCGGCGCCCTGCTCC 68
           ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     1 CCGCATGGCTCCCCGTGCCCCAGCCCC  GGCTCCTGGCTCCCGTGCCCCCTGCCCCGGCGCCCTGCTCC 60

Qy    69 AGGCCTCACTGTGCAACTGCTGCTGCTGTCCATCCCCAGAG 128
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Db    61 AGGCCTCACTGTGCAACTGCTGCTGTCCATCCCCAGAG 120

Qy   129 GTTGCCCCCGGATGCAGGAGGATTCCCCCTTGGGGAGGAGAGATGACC 188
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTTGCCCCCGGATGCAGGAGGATTCCCCCTTGGGGAGGAGAGATGACC 180

Qy   189 ACTGGGGCGAGGGAGGAGTCTGCCCAGTGAAGGAGGAGGATCACCCACCCGG 248
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Db   181 ACTGGGGCGAGGGAGGAGTCTGCCCAGTGAAGGAGGAGGATCACCCACCCGG 240

Qy   249 AGAGGAGGGATCTACCTGGAGAGGAGGAGGATCTACCTGAAGTTAA 308
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Db   241 AGAGGAGGGATCTACCTGGAGAGGAGGAGGATCTACCTGAAGTTAA 300

Qy   309 GCCTAAAACAGAGAAGAGGAGGGCTCCCCTGAAGTTAGAGGATCTACCTAGTTGTTGAGGGCTCC 368
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Db   301 GCCTAAAACAGAGAAGAGGAGGGCTCCCCTGAAGTTAGAGGATCTACCTAGTTGTTGAGGGCTCC 360

Qy   369 TGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGATGACCAGAG 428
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Db   361 TGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGATGACCAGAG 420

Qy   429 TCATTGGGGCCTATGGAGGCGACCCGGCCCTGGCCCTGGCCGGGTGTCCCCAGCCTGGCGGGCCG 488
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Db   421 TCATTGGGCGCTATGGAGGCGACCCGGCCCTGGCCCTGGCCGGGTGTCCCCAGCCTGGCGGGCCG 480

Qy   489 CTTCCAGTCCCCGGTGGATATCCGGCCCCCTTCTCTGCCCCAGCGCTGCGGCCGGCCCTGCGCCC 548
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CTTCCAGTCCCCGGTGGATATCCGGCCCCCTTCTCTGCCCCAGCGCTGCGGCCGGCCCTGCGCCC 540

Qy   549 CCTGGGAACTCCTGGGCCTTCCAGCTCCCCAGAACTGCGCCTGCCGGAACAATGG 608
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCTGGGAACTCCTGGGCCTTCCAGCTCCCCAGAACTGCGCCTGCCGGAACAATGG 600

Qy   609 CCACAGTGTGCAACTGACCCTGCCTCCTGGGGCTCTGAGGATGGCTCGGGGTCCCCGGGGA 668
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CCACAGTGTGCAACTGACCCTGCCTCCTGGGGCTCTGAGGATGGCTCGGGGTCCCCGGGGA 660

Qy   669 GTACCGGCGGCTCTCGACGTCGCACTGGGGACGTCCAGGTGTCGTCGGGGGCTCGGAGCA 728
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Db   661 GTACCGGCGGCTCTCGACGTCGCACTGGGGACGTCCAGGTGTCGTCGGGGGCTCGGAGCA 720

Qy   729 CACTGTGGAAGGCCACGCGTTTCCTGCCGAGATCCACGTGGTTCACCTCAGCACCGGCTT 788
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Db   721 CACTGTGGAAGGCCACGCGTTTCCTGCCGAGATCCACGTGGTTCACCTCAGCACCGGCTT 780

Qy   789 TGCCAGAGTTGACGAGGCCTTGGGGGGGCGGGGGCGGAGGCCTGGGTGTTGGCCGGCCTTTCT 848
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Db   781 TGCCAGAGTTGACGAGGCCTTGGGGGGCGGGGGCGGAGGCCTGGGTGTTGGCCGGCCTTTCT 840

Qy   849 GGAGGAGGGGCCCGGAGAGAAAACAGTGCCTATGAGCAGTTGCCTATGAGCAGTTGAAGAAAT 908
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGAGGAGGGGCCCGGAAGAGAAAACAGTGCCTATGAGCAGTTGCCTATGAGCAGTTGAAGAAAT 900

Qy   909 CGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGAGACTCAGGTCCCAGAGAATCGCACTCCTGCCCTC 968
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CGCTGAGGAAGGCTCAGGACTCAGGTCCCAGAGACTCAGGTCCCAGAGAATCGCACTCCTGCCCTC 960

Qy   969 TGACTTCAGCGCCTACTTCCAATATGAGGGGGTTCTGACTACACCGGCCCGTGCCCAGGG 1028
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Db   961 TGACTTCAGCCGCTACTTCCAATATGAGGGGGTTCTCGACTACACCGGCCCGTGCCCAGGG 1020

Qy  1029 TGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGCTGAAGCAGCTCCACACCCT 1088
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Db  1021 TGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGCTGAAGCAGCTCCACACCCT 1080

Db  1021 TGTCATCTGGACTGTGTTTAACCAGACAGTGATGATGCTGCTGAAGCAGCTCCACACCCT 1080
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Qy  1089 CTCTGACACCCCTGGGGGACCTGGTGACTTCCTCGCTACAGCTGAAACTTCCGACGGACGCA 1148

Db  1081 CTCTGACACCCCTGGGGGACCTGGTGACTTCCTCGCTACAGCTGAAACTTCCGACGGACGCA 1140
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Qy  1149 GCCCTTTGAATGGGCGGAGTGAGTTGAGGCCGTCTCCTGCTCGTGGTGGACGAGCAGTCCTCG 1208

Db  1141 GCCCTTTGAATGGGCGGAGTGAGTTGAGGCCTCCTTCCTTCCCTGCTCGTGGTGGACGAGCAGTCCTCG 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1209 GGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCCTGGGTGGCATCCTCAGCGCCTGGT 1268

Db  1201 GGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCCTGGGTGGCATCCTCAGCGCCTGGT 1260
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Qy  1269 TTTTGGGCCTCCTTTTTTGCTTGTCACCAGGGTCCGGTTCCTTGTCCAGATGTGAGATGGCAGCA 1328

Db  1261 TTTTGGGCCTCCTTTTTTGCTTGTCACCAGGGTCCGGTTCCTTGTCCAGATGTGAGATGGCAGCA 1320
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Qy  1329 CAGAAGGGGGAACCAAAAGGGGTGTGAGCTACCCGCCAGAGGTAGCCGAGACTGGGAGC 1388

Db  1321 CAGAAGGGGAACCAAAAGGGGTGTGAGCTACCCGCCAGAGGTAGCCGAGACTGGGAGC 1380
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Qy  1389 CTAGAGGGCTGGGATCTTGGAGAAATGTGAGAAGCCCAGAGGGGGGGGGGGGGGAGCCCG 1448

Db  1381 CTAGAGGGCTGGGATCTTGGAGAATGTGAGAAGCCCAGAGGGGGGGGGGGGGGAGCCCG 1440
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Qy  1449 TAACTGTCCTGTCCTCGTCTCATTATGCCAC 1477

Db  1441 TAACTGTCCTGTCCTCGTCTCATTATGCCAC 1469
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RESULT 4
LOCUS   CR590646   1492 bp   mRNA   linear   HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DJ005YK14 of T cells (Jurkat cell line)
            Cot 10-normalized of Homo sapiens (human).
ACCESSION   CR590646
VERSION   CR590646.1 GI:50471453
KEYWORDS   HTC; CNSLT_cDNA.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1492)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK   Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue
REFERENCE   2 (bases 1 to 1492)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
     source   1..1492
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ005YK14"
                     /tissue_type="T cells (Jurkat cell line) Cot
                     10-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match 93.5%; Score 1423.4; DB 3; Length 1492;

Best Local Similarity   98.1%; Conservative   0; Pred. No. 0;
Matches 1461; Mismatches   1; Indels   27; Gaps   1;

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Qy      1 ACAGTCAGCCGCAATGGCTCCCCGTGCCCCTGCCTCCCTCTGTTGATCCCGGC 60
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Db     31 ACAGTCAGCCGCAATGGCTCCCCGTGCCCCTGCCTCCCTCTGTTGATCCCGGC 90

Qy     61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTGCTGCTTCGCTGTGCCTGTGCCAT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     91 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTGCTTCGCTGTGCCTGTGCCAT 150

Qy    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGAGTGCTCTTCTCGGGGAA 180
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    151 CCCCAGGAGGTTGCCCCGGATGCAGGAGGAGTGCTCTTCTCGGGGAA 210

Qy    181 GATGACCCACTGGGCGGAGGGATCTGCCCAGTGAAGAAGGATTCACCCAGAGGAGGAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GATGACCCACTGGGCGGAGGGATCTGCCCAGTGAAGAAGGATTCACCCAGAGGAGGAT 270

Qy    241 CCACCCGGAGGAGGAGATCTACCTGGAGGAGGAGGATCTACCT 300
            |||||||||||||||||||||||||||||||||||||||||||
Db    271 CCACCCGGAGGAGGAGATCTACCTGGAGGAGGAGGATCTACCT 330

Qy    301 GAAGTTAAGCCTAAATACAGAAGAAGAGAGAGAGGGCTCCCTGAAGTTAGAGGACTACTACTGTT 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GAAGTTAAGCCTAAATCAGAAGAAGAGAGAGGGCTCCCTGAAGTTAGAGGACTACTACTGTT 390

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAGAAGGGGAT 450

Qy    421 GACCAGGAGTCATTGGGAGGCGGCTATGGAGGGGGCAAAAAGAAGGGGGAT 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 GACCAGAGTCATTGGGCGTATGGAGGGGCAACCCGGGTGTCCCCAGCCTGC 510

Qy    481 GCGGGCGCCGCTTCAGTGCCCGGTGGATATCCGCGCCCCAGCTCGCGCGCCCGGCGCC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GCGGGCGCCGCTTCCAGTCCCCGGATATCCGCGCCCCAGCTCGCGCGCCCGGCGCC 570

Qy    541 CTGCGCCGCCCCCTGGAAACTCCTGCGCTTCCAGCGCTCCCGCGCCTCCCGCGGCCCGCGC 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 CTGCGCCGCCCCCTGGAAACTCCTGCGCTTCCAGCGCTCCCGCGCCTCCCGCGGCCCGCGC 630

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTGCCTCCTGGGCTAGAGGTCCC 660
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Db    631 AACAATGGCCACAGTGTGCAACTGACCCTGCCTGCCTCCTGGGCTAGAGGTCCC 690

Qy    661 GGGCCGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGCAGGTCGTCCGGGC 720
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Db    691 GGGCCGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACTGCAGGTCGTCCGGGC 750

Qy    721 TCGGGAGCACACTGTGGAAGGCCACACGGTTCCCTGCCAGATCCACGTGTCACTCGACTC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 TCGGAGCACACTGTGGAAGGCCACACGGTTCCCTGCCAGATCCACGTGTCACTCGACTC 810

Qy    781 ACGGCCTTTGCCAGTTGACGAGGGCGAGGCCTGGGCCTGGCC 840
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Qy    841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGCTGCTCGGCTTG 900
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Db    871 GCCTTTCTGGAGGAGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTTGCTGCTGCTCGGCTTG 930

Qy    901 GAAGAAATCGCTGAGGAAGCTCAGGATCTCAGGTCCCAGGACTGGACATATCTGCACTC 960
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Db    931 GAAGAAATCGCTGAGGAAGCTCAGGATCTCAGGTCCCAGGACTGGACATATCTGCACTC 990

Qy    961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGGTGGTCTCTGACTACACGCCCCTGT 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGGTGGTCTCTGACTACACGCCCCTGT 1050

Qy   1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGGTGCTGCTAAGAGCAGCTC 1080
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Db   1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGGTGCTGCTAAGAGCAGCTC 1110
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(sequence continues)

RESULT 5
AL542336
LOCUS   AL542336   1084 bp   mRNA   linear   EST 24-MAR-2004
DEFINITION   AL542336 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YB19
               5-PRIME, mRNA sequence.
ACCESSION   AL542336
VERSION   AL542336.3 GI:45717912
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1084)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:30547384.
               Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
               1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
               end enriched, double-strand cDNA was digested with Not I and cloned
               into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
               was not normalized. Library was constructed by Life Technologies, a
               division of Invitrogen.
               This sequence belongs to sequence cluster 8734.f.
               For more information about this cluster, see
               http://www.genoscope.cns.fr/cdna?s=CS0DE010CA10QP2&c=8734.f.

FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE010YB19"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."

ORIGIN

Query Match   67.3%;   Score 1024.8;   DB 1;   Length 1084;
Best Local Similarity   98.4%;   Pred. No. 4.6e-247;
Matches 1045;   Conservative   9;   Mismatches   6;   Indels   2;   Gaps   2;

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Qy      1 ACAGTCAGCCGCATGGCTCCCCGTGTGCCCCAGCCCTGGCTCCCCTTGTTGATCCCCGGCC 60
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Db     12 ACAGTCAGCCGCATGG--TCCCCGTGTGCCCCAGCCCTGGCTCCCCTTGTTGATCCCCGGCC 70

Qy     61 CCTGCTCCAGGCCTCACTGTGCAAACTCGCTGCTTGCTGTTCTGATGCCTGTCCAT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CCTGCTCCAGGCCTCACTGTGCAAACTCGCTGCTTGCTGTTCTGATGCCTGTCCAT 130

Qy    121 CCCCAGGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CCCCAGGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGGGAGGAGGCTCTTCTGGGGAA 190

Qy    181 GATGACCCACTGGGCGACGAGGATCTCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 GATGACCCACTGGGCGACGAGGATCTCCCAGTGAAGAGGATTCACCCAGAGGAGGAT 250

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(sequence alignment continues)

ORIGIN

Query Match   60.5%;   Score 920.8;   DB 1;   Length 1070;
Best Local Similarity   96.4%;   Pred. No. 7.6e-221;
Matches 991;   Conservative   13;   Mismatches   15;   Indels   9;   Gaps   6;

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(sequence alignment continues)

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Db   330 GAAGTTAAGCCTAAATCAGAAGAAGAGAAGAGGGGCTTCCCTGAAGTTAGAGGATCTACTACTGTT 389

Qy   361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
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Db   390 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 449

Qy   421 GACCAGAGTCATTGGCGCTATGGAGGCGGAGGACCCGGCCCCTGGCCCTGGCGTGTCCCCAGCCTGC 480
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Db   450 GACCAGAGTCATTGGCGCTATGGAGGCGGAGGACCCGGCCCCTGGCCCTGGCGTGTCCCCAGCCTGC 509

Qy   481 GCGGGCCGCGCCTTCCAGTCCCCGGGTGGGAT ATCCGCGCCCGCCTTCTCCGGCC 540
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Db   510 GCGGGCCGCGCCTTCCAGTCCCCGGGTGGGAT ATCCGCGCCCGCCTTCTCCGGCC 569

Qy   541 CTGCGCCCCCCCTGGAACTCCTGGGCTTCCAGTCTCCAGACTCCCAGCCTCCCAGAACTGCGCCCTGGGC 600
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Db   570 CTGCGCCCCCCCTGGAACTCCTGGGCTTCCAGTCTCCAGACTCCCAGCCTCCCAGAACTGCGCCCTGGGC 629

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Qy   661 CTCGGGAGCACACTGTGGAAGGCTCAGCTGCATCTCCAGATCCACGTTGGTTCACCTCAG 719
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Db   690 CTCGGGAGCACACTGTGGAAGGCTCAGCTGCATCTCCAGATCCACGTTGGTTCACCTCAG 749

Qy   720 CTCGGGAGCACACTGTGGAAGGCTCAGCTGCATCTCCAGATCCACGTTGGTTCACCTCAG 779

Qy   750 CTCGGGAGCACACTGTGGAAGGCTCAGCTGCATCTCCAGATCCACGTTGGTTCACCTCAG 809

Qy   780 CACCGGCCTTTGCCAGAGTTGACGAGGGCCACCGTTTCCCTGCCGAGATCCACGTTGGTTGGC 839

Db   810 CACCGGCCTTTGCCAGAGTTGACGAGGGCCACCGTTTCCCTGCCGAGATCCACGTTGGTTGGC 869

Qy   840 CGCCTTTCTGGAGGAGGGCCCCGGGAGAAGAAACAGTGCTCTATGAGCAGTTGCTCGTTCGGCTT 899

Db   870 CGCCTTTCTGGAGGAGGG-CCGGRAGAAACAGTGCCTATGAGCAGTTGCTCGTTTCGGCTT 928

Qy   900 GGAAGAAATCGCTCAGAGGAGGAGCTCAGAGGACTCAGGTCCCAGGACCATATCTGCACT 959

Db   929 GGAAGAAATCGCTCGAGGAA-GCTCAGAGGACTTAGGKYCCAGGACTGGACAGAAAATCTGCACT 987

Qy   960 CCTGCCCCTCTGACTTCAGCGGGCGCTACTTCCAATATGAGGGGGTCTCTGACTACACCGCCCCTG 1019

Db   988 C--TGSCTCTGACTTCAG-CGCTAMTTCCAWAWGAGGGTCTCT---KAtWMACCGCCCCTK 1041

Qy  1020 TGCCCAGG 1027
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Db  1042 TGCCAGGG 1049
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ORIGIN

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Query Match    59.4%;  Score 903.4;  DB 1;  Length 1009;
Best Local Similarity   99.1%;
Matches  956;  Conservative   4;  Mismatches   0;  Indels   5;  Gaps  5;
                    Pred. No. 1.8e-216;

Qy    1 ACAGTGCAGCGCAGCATGGCTCCCCGTGCCCCAGCCGCCCTCCCTCGTTGATCCCGGCC 60
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Db   31 ACAGTGCAGCGCAGCATGGCTCCCCGTGCCCCAGCCGCCCTCCCTCGTTGATCCCGGCC 90

Qy   61 CCTGCTCCAGGGCCTCACTGTGCAACTGCTGCTGTCGTCACTGCTTCGTGATGCCTCCAT 120
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Qy  121 CCCCAGAGGTTGCCCCGGATGCAGGAGGAATTCCCCTTGGGAGGAGGGCCTTCTGGGGAA 180
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Qy  181 GATGACCCACTGGGCGGAGGAGGATCTGCCCAGTGAAGAGGATCACCCAGAGGAGGAT 240
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Qy  241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGATCTACCT 300
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Qy  301 GAAGTTAAGCCTAAATCAGAAGAAGAGAAGGGGCTTCCCTGAAGTTAGAGGATCTACTACTGTT 360
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Db  331 GAAGTTAAGCCTAAATCAGAAGAAGAGAAGGGGCTTCCCTGAAGTTAGAGGATCTACTACTGTT 390

Qy  361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  391 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAATGCCCACAGGGACAAAAGAAGGGGAT 450

Qy  421 GACCAGAGTCATTGGCGCTATGGAGGCGGAGGACCCGGCCCCTGGCCCTGGCGTGTCCCCAGCCTGC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  451 GACCAGAGTCATTGGCGCTATGGAGGCGGAGGACCCGGCCCCTGGCCCTGGCGTGTCCCCAGCCTGC 510

Qy  481 GCGGGCCGCGCCTTCCAGTCCCCGGGTGGGATATCCGCGCCCGCCTTCTCCGGCC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  511 GCGGGCCGCGCCTTCCAGTCCCCGGGTGGGATATCCGCGCCCGCCTTCTCCGGCC 570

Qy  541 CTGCGCCCCCCCTGGAACTCCTGGGCTTCCAGTCTCCAGACTCCCAGCCTCCCAGAACTGCGCCCTGGGC 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  571 CTGCGCCCCCCCTGGAACTCCTGGGCTTCCAGTCTCCAGACTCCCAGCCTCCCAGAACTGCGCCCTGGGC 630

Qy  601 AACAATGGCCACAGTGTGCAACTAACCCTGCCTCCTGCTAGAGATGGCTCTGGGGTCCC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  631 AACAATGGCCACAGTGTGCAACTAACCCTGCCTCCTGCTAGAGATGGCTCTGGGGTCCC 690
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RESULT 8

LOCUS   BX423970   916 bp   mRNA   linear   EST 03-MAY-2004
DEFINITION   BX423970 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
           CS0DA003YB12 5-PRIME, mRNA sequence.
ACCESSION   BX423970
VERSION   BX423970.2 GI:46955310
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 916)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30765328.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
          was not normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
          This sequence belongs to sequence cluster 5300.f
          For more information about this cluster, see
          http://www.genoscope.cns.fr/cdna?s=CS1DA001Z09QP1&c=5300.f.
FEATURES   Location/Qualifiers
    source   1..916
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="CS0DA003YB12"
               /tissue_type="NEUROBLASTOMA"
               /clone_lib="Homo sapiens NEUROBLASTOMA"
               /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
               with a NotI-oligo(dT) primer. Five prime end end enriched,
               double-strand cDNA was digested with Not I and cloned into
               the Not I and EcoRV sites of the pCMVSPORT 6 vector.
               Library was not normalized."

Query Match   58.6%; Score 891.4; DB 5; Length 916;
Best Local Similarity 96.4%; Pred. No. 1.9e-213;
Matches 883; Conservative 23; Mismatches 10; Indels 0; Gaps 0;

ORIGIN

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Qy       661 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCCATCTTGCACTGGGGGGGCTGCAGGTCGTCGTCCCGGGC 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       691 GGGCGGGGAGTACCGGGGCTCTGCAGCTGCCATCTGGGGGGGCTGCAGGTCGTCGTCCCGGGC 750

Qy       721 TCGGAGCACACTGTGGGAAGGCCACCGTTTCCCTGCCGAGATCTCACGTGGTTCACCTCAGC 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       751 TCGGAGCACACTGTGGGAAGGCCACCGTTTCCCTGCCGAGATCTCACGTGGTTCACCTCAGC 810

Qy       781 ACCGGCCTTTGCCAGAGTTGACAGAGGCCTTGTCGGGGGCGGGGAGGCGGGCGGCTGTCTGGCC 840
             ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db       811 ACCGGCCTTTGCCAGAGTTGACAGAGGCCTTGTCGGGGGCGGGGAGGCGGGCGGCTGGTCTGGCC 869

Qy       841 GCCTTTCTGGAGCGAGGAGGGGCCCGGAAGAAAAACAGTGCCTATGAGCGAGTTGCTGTGCTTG 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       870 GCCTTTCTGGAGCGAGGAGGGGCCCGGAAG-AAACAGTGCCTATGAGCGAGTTGCTGTGCTTG-C 928

Qy       901 GAAGAAATCGCTGAGGAGGAGGCCTCAGGATCCCAGGACTGGACATATCTGCACTC 960
             ::||||||||||||||||||||||||||||||||||||:|:||:||||||||||||
Db       929 GAA-RAATCGCTGAGGAA-GCTCAGAGACTCAGGKCCCCAGGACAWAT-TGCACTC 985

Qy       961 CTGGCC 965
             ||||||
Db       986 CTGGCC 990
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RESULT 9

LOCUS   AL554665   1071 bp   mRNA   linear   EST 30-MAR-2004
DEFINITION   AL554665 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
           clone CS0DI085YF18 3-PRIME, mRNA sequence.
ACCESSION   AL554665
VERSION   AL554665.3 GI:45859416
KEYWORDS   EST.

RESULT 9
AL554665/c

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Qy         9 CCGCATGGCTCCCCTTGTGCCCCAGCCCTGGCTCTTCCCCCTTTGTTGTTGTTGATTCCCGGCTCCTGCTCC 68
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db         1 CCGCATGGCTCCCCTGTCGCCCCAGCCCTGGCTCTTCCCCCTCTGTTGAWCCCGGCTCC 60

Qy        69 AGGCCTCACTGTGCCAACWGGCTGCTACTCCTTCTGATGCCGTCGTCCATCCCCAGAG 128
             |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        61 AGGCCTCACTGTGCCAACWGGCTGCTACTCCTTCTGATGCCGTCGTCCATCCCCAGAG 120

Qy       189 ACTGGGGCCGAGGAGGATCTTGCCCCAGTGAAGAGGAGGAGGATTCACCCAGGAGGAGGAGGATCCACCCGG 248
             |||||||||||||||||||||||||||||||||||||||||||||||:|||:|||||||||||||||||
Db       181 ACTGGGGCCGAGGAGGATCTTGCCCCAGTGAAGAGGAGGAGGATTCACCCAGGAGGAGGAGGATCCACCCGG 240

Qy       249 AGAGGAGGATCTACCTGGAGGAGGATCTTACCTGGAGGAGGATTCACCTGGAGGAGGATCTGAAGTTAA 308
             ||||||||||||||||||||||||||||||||||||||||:||:||||||||||||||||||||
Db       241 AGAGGAGGATCTTACCTGGAGGAGGATCTTACCTGGAGGAGGATCTWACCTGAAGTTAA 300

Qy       309 GCCTAAATCAGAAGAAGAGAGGAGGCTCCCTGAAAGTTAGAGAGAGTCTGTTGAGGCTCC 368
             ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db       301 GCCTAAATCAGAAGAAGAGAGGAGGCTCCCTGAAAGTWAGAGAGGATCTACCTACTGTTNGAGGCTCC 360

Qy       369 TGGAGATCCTCAAGAAACCCCAGAATAATGCCCACAGGAGACAAAGGAAAGGGGGATGACCAGAG 428
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGAGAACCTCAAGAAACMCCACAGGGAATAAWGCCCACAGGGAGACAAAGGAAAGGGGGATGACCAGAG 420

Qy       429 TCATTGGCGGCTATGGAGGCGGACCCGCGCTCCGGCCCCGGGGTGTCCCCAGCCTGCTGGCGCGGGCG 488
             |||||||||||||:|||||||||||||||||||||||||||:|||||||||||||||||||
Db       421 TCATTGGCGGCGATGGAGGCGGACCCGCGCCCGGCCCCGGGGTGTCCCCAGCCTGCTGGCGCGGGCG 480

Qy       489 CTTCCAGTCCCCGGTGGGATTATCCGGCCCCCCAGCTCGCCCGCTTCTGCCCCGGCCCCTGCGCC 548
             ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db       481 CTTCCAGTCCCCGGTGGATATCCCAGCTCGCCCGCTTCTGCCCGCCCCTTTGCGCCCCCTGCGGC 540

Qy       549 CCTGGAACTTCCTGGGGCTTCCAGCTCCCCGCCGCCGCTCCCCGGAGAACTCGCGCCCGTGGCAACAATGG 608
             |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db       541 CCTGGAACTTCCTGGGGCTTCCAGCTCCCCGGCGCTCCCCAGAACTCGGCGMACAATGG 600

Qy       609 CCACAGTGTGCAACTGACCCTGCCTTCCTGGGGCTTAGAGATGGGCGTCCCGGCGGGGA 668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CCACAGTGTGCAACTGACCCTGCCTTCCTGGGGCTTAGAGATGGGCGTCCCGGCGGGGA 660

Qy       669 GTACCGGGGCTCTGCACTGGGGGGGCTGCAGGTGCGTGCTCGGGAGCA 728
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Db       661 GTACCGGGGCTCTGCAGCTGCCATCTGGGGGGGCTGCAGGTGCGTGCTCGGGMACAATGG 720

Qy       729 CACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACCACTGGTTCACCTCAGCACCGCCTT 788
             |||||||||||||||||||||||||||||||||||:||:||||||||||||||||||||
Db       721 CACTGTGGAARGCCACCGTTTCCCTGCCGAGATCCACGTGGTTYAMCTCARCACCGCCTT 780

Qy       789 TGCCAGAGTTGACAGAGGCCTTGGGGGCGCGGGGAGGCGGGCTGGGCCGGCCGCCTTTCT 848
             |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db       781 TGCCAGARATTGAMGAGGGCCTTGGGGGCGCGGGAGGCGGGCTGGGCCGGCCGCCTTTCT 840

Qy       849 GGAGGAGGGGCCCGAAGAGAAAACAGTGCCTATGAGCAGTTGCTGTGCTTCGCTTGGAAGAAAAAT 908
             |||||||||||||||||:|||||||.|||||||||:||||||||:|||||||||||||||:
Db       841 GGAGGAGGGGCCCGGAAGAAAAAAMAATRCCTATRAACAGTTGCTGTTTCGCTTGGGAAAAW 900

Qy       909 CGCTGAGGAGAAGGCTCA 924
             ||||||||||||||||||
Db       901 MGCTGAGGAGAAGGCTCA 916
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SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1071)
AUTHORS   Li,W.B.; Gruber,C.; Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:31276475.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5300.f.
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0D1085DC09NP1&c=5300.f.
FEATURES   Location/Qualifiers
     source   1..1071
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /clone="CS0D1085YP18"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /note=1st strand cDNA was primed with a NotI-oligo (dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match   56.6%;   Score 861.6;   DB 1;   Length 1071;
Best Local Similarity 93.6%;   Pred. No. 6.4e-206;
Matches 1003;   Conservative 21;   Mismatches 31;   Indels 17;   Gaps 12;

Qy   451 CCGGCCCGGCCCCCGGGGTGTCCCCAGCCTTCCAGTCTCCCGGTGGATATC 510
          |||| ||||| ||| ||||||||||||||||||||||||||||||||||
Db 1066 CCCGCCCTTGSCCCSGGTGTCCCCAGCCCTGCGC--CGCCGGCTHCMAGTCCCGGT-GATATC 1009

Qy   511 CGCCCCCAGCTCGGCCCTTCTGCCCCGGCCCCTGGAACTCCCTGGGCTTCCAG 570
          |||||| |||||||||||| || ||||||||||||||||||||||| |::|
Db 1008 CGCCCCCRG-TYGCCGCCTTCTGCCCCG--CCYGCGCCCCYTGGA--CTCCTGGSTTCCVG 953

Qy   571 CTCCGGCCGGCTCCCAGAACTGCGCCCTGCCCAACAAATGCCACACGTGTCCACACCCTG 630
          |||:| ||| |||| ||||| ||||||| ||| |||||||| || || ||||||
Db   952 STCCCGSCCGCTCCCAGGRACTGCG--CTGCGCAACAAATGGCCACAGTGTGCAAACTGACCCTG 894

Qy   631 CCTCCCTGGGCTAGAGATGGCGCTCTGGGGTTCGGGGTCTCGAGCTGCAGCTGCGAT 690
          |||||| ||||||||| || ||| |||||||| ||| ||||| ||||| |||||||
Db   893 CCTCCCTGGGCTAGAGATGGCTCTGGGTCCCGGCGCGGAGTTCCCGCGCTCTGCAGCTGCAT 834

Qy   691 CTGCACTGGGGGGCCTGCAGGTCGTCCGGAGCGCACAGTCGGCGCCACCGTTTC 750
          ||||||||||||||||||||||||| ||||| ||| || |||| |||||||||
Db   833 CTGMACTGGGGGGCTCGCAGGTCGTCCGGCGRGCACAYGTGCAGGCCACCGTTTC 774

Qy   751 CCTGCCGGAGATCCACGTGGTTCACCTCAGCACCGCCCCCTTTGCCAGCAGGCCTTG 810
          |||||||||||||||||| | ||| ||||||||| ||| |||||||| ||||||||
Db   773 CCTGCCGAGATCCACGTGGTTCACCTCAGCACCGCCCTTTGCCAGAGTTGACGAGGCCTTG 714

Qy   811 GGGGCGCCCCCGGAGGCCCTGGGCCGTRGTTGGCGCGGAGAGGCCCCGGAAGAGAAAAC 870
          |||||||||||||||||||||||| ||||||||||||||| ||||||| |||||||||
Db   713 GGGGCGCCCCCGGAGGCCCTGGGTCGCGGTGTTGGCGCCCGCTTTCTGGAGAGGAGGAAAAC 654

Qy   871 AGTGCCTATGAGAGAGCAGTTGCTGTTCTGCCTGGGGAAGAAAATCGCTAGGAGGCTCAGAGACT 930
          ||||| ||||||||| || |||||| ||||||||| ||||||||| |||||||||||||||||
Db   653 AGTVGCCTATGAGAGCAGTGGCTSTCTCGCCTTGGCTGGAAGMAATCGCTAGGAGGCTCAGAGACT 594

Qy   931 CAGGTCCCAGGGACT--GGACATAYCTGCACTCCT-GCCCTCTGACTTCAGCCG-CTACTT 986
          ||||||||||||||| || ||||||||||||||| |||||||||||||||||| |||||
Db   653 ...

Db   593 CAGGTCCCAGCACTCGCCGACATCTCTGCGACTTCGCACTTCAGCCCGCCCACTT 534

Qy   987 CCAATATGAGGGGRTCTCTGACTACTACACCGCGCCCTGTGTCCCCAGGGTGTCATCTGGACTGGTTT 1046
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |||||
Db   593 CCAATATGAGGGGRTCTCTGACTACTACACCGCGCCCTGTGTCCCCAGGGTGTCATCTGGACTGGTT 474

Qy 1047 TAACCACAGACAGTGGAATGCTGAGTGTGTPAAGCAGCTCCACACCTCTTCTGACACCCTGTGGGG 1106
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   473 TAACCACAGACAGTGGATGCTGAGTGTGTAAGCAGCTCCACACCTCTTCTGACACCCTGTGGGG 414

Qy 1107 ACCTGGTGACTTCTCGGGCTACAGCTGAACTTCCGGCGGCGGCGGCAGCAGCCTTTGAAATGGGCGGAGT 1166
          |||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   413 ACCTGGTMACTCTCGGGCTACAGCTGAACTTCCGGCGGCGGCGGCAGCAGCCTTTGAAATGGGCGGAGT 354

Qy 1167 GATTGAGGGCCTTCCTTCCCTGCTGGGACGTGGGACAGCAGCAGTCTCCTGGGCGGCTGAGCCAGTCCA 1226
          ||||||||||||||||||||| |||||||||||||||||||||||||| |||||||||||||||||||
Db   353 GATTGAGGGCCTTCCTTCCCTGCTGGGACGTGGGACAGCAGCAGTCCTGGGCGGCTGAGCCAGTCCA 294

Qy 1227 GCTGAAATTCCTGCCCTGGGCGTGCTGGTGACATCCTAGCCCCTGGTTTTTTTGGTTTTTTTGC 1286
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Db   293 GCTGAAATTCCTGCCCTGGTCTGGTGACATCCTAGCCCCTGGTTTTTTTGGGCTCTTTCTTTTGGC 234

Qy 1287 TGTCACCAGGGTCGGGTTCCTTGTGCAGRATGAGRAGGCACAGCTACGAGAAGGGAACCAAAGG 1346
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   233 TGTCACCAGGGTCGGGTTCCTTGYGGTGCAGATGAGDATGAGAAGGCCAGCAGCACAGAAAGGGAACCAAAGG 174

Qy 1347 GGGGTGTGAGCTACCCGCCACCAGAGGTAGCGGAGACTGGAGC---CTAGAGGGCTGGATCT 1403
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Db   173 GGGGTGTGAGCTACCCGCCCCCACCAGAGAGGTAGCCGGAAACTGGAGCACTAGAGGACCATGGATCT 114

Qy 1404 TGGGAGAAATGTTGAGAAG--CCAGCCAGGAGCGCATCTGAGGGGGGGGGGCGGTAACTGTGTCCTGTC 1461
          ||||||||||||||||||| |||||||||||||||||| ||| ||||||||||||||||| |||||
Db   113 TGGAGAATGTTGAGAAGACACAGGAGGGCATCTGAGGGGGGGGGGCGGGTNACTGTGTCCGTGTC 54

Qy 1462 CTGCTCATTATG--CCACTTCCTTTTTNAACTGCCAAGAAAAAATTTTTAAAAATAAA 1512
          |||||||||||| |||| |||||||||||| :: ||||||||||||||||||||||
Db   53 CTGCTCATTATGNCCACTYCCTTTTTTNACTGCCAAANNMMWVTTTTAWWATTA 2

RESULT 10
BX401186
LOCUS   BX401186   1017 bp   mRNA   linear   EST   29-APR-2004
DEFINITION BX401186 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.
ACCESSION   BX401186
VERSION   BX401186.2 GI:46876709
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1017)
AUTHORS   Li,W.B.; Gruber,C.; Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 13, 2003 this sequence version replaced gi:30626393.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5300.f.
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DK009DH05QP1&c=5300.f.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"

ORIGIN
/clone="CS0DK009YP10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match   Best Local Similarity   54.7%;   Score 832; DB 5; Length 1017;
Matches 896; Conservative   3; Mismatches 13; Indels   8; Gaps   5;

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Qy      1 ACAGTCAGCCGCCATGGCGTCCCCCTGTGCCCCAGCCCTGTCCTCCTCTGTTGATCCCGGCC 60
          ||||||||||||||||||||:||:||||||||||||||||||||||||||||||||||||||
Db      2 ACAGTCAGCCGCCATGG-TCCCCTGTGCCCCAGCCCTGTCCTCCTCTGTTGATCCCGGCC 60

Qy     61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTCTGCTCTCACTGCTCTTCTGATGCCTGTCCAT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTCTGCTCTCACTGCTCTTCTGGTGCCTGTCCAT 120

Qy    121 CCCCAGCGAGGTTGCCCCCGGATGCAGGAGGAGGAGTTCCCCCTTGGGAGGAGGCTCTTCTGGGGGAA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGCGAGGTTGCCCCCGGATGCAGGAGGAGGAGTTCCCCCTTGGGAGGAGGCTCTTCTGGGGGA 180

Qy    181 GATGACCCACTGGGCGACGGAGGAGGATCTGCCCCAGTGAAGGAGGATCCACCCAGAGAGAGGAGGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GATGACCCACTGGGCGACGGAGATCTGCCCCAGTGAAGGAGGATCACCCAGAGAGAGGAGGAT 240

Qy    241 CCACCCCGGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCT 300
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Db    241 CCACCCCGAGGAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCT 300
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Qy    901 GGAGAAATCGCTGAGGAGG 920
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Db    894 GGWAGAAATCGCTGAGGAGG 913
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RESULT 11
LOCUS   BX423969/c   961 bp   mRNA   linear   EST 03-MAY-2004
DEFINITION   BX423969 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
             CS0DA003YB12 3-PRIME, mRNA sequence.
ACCESSION   BX423969
VERSION   BX423969.2   GI:46954391
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 961)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30766327.
             Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
             1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
             was not normalized. Library was constructed by Life Technologies, a
             division of Invitrogen.
             This sequence belongs to sequence cluster 5300.f.
             For more information about this cluster, see
             http://www.genoscope.cns.fr/cdna?s=CS1DA001ZF09NP16c=5300.f.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DA003YB12"
                     /tissue_type="NEUROBLASTOMA"
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                     /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

Query Match   Best Local Similarity   53.5%;   Score 813.6; DB 5; Length 961;
Matches 852; Conservative   24; Mismatches 71; Indels   3; Gaps   2;

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Qy    513 CCCCCAGCTCGCGCGCCTTTCTGCCCGCCTGGGCCCCCTGGGAACTCCTGGCGTTCCCAGCT 572
          |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CCSCCCCCGSTCCGCCCCYTTTKCCCGGCCGGSGCCCCCYYGKA--CTCTTGKGTTCCWGBT 904

Qy    573 CCCGCCCGTCCCAGAACTGCGGCTGCGCAACAAATGGCCACAGTGTGCAACTGACCCTGCC 632
          ||||:||||||||:|||||||||||||||||||:||:||||:||:|||||||||||||
Db    903 CCCCKGKCTCCYAGAACYCG-CTGGGCGCYATAAATGGCYACAGTGKGCYAYTRACCCTCCC 845
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```
Qy    633 TCCTGGGCTAGAGATGGCCTCTGGGTCCCGGGCCGGAGTACCGGGCCTCTCGCAGCTGCATCGT 692
          |||||||||||||||||||||||||||||||||||||||:|||||||||||||:||:|||||
Db    844 TCCTGGGCTTATAGATGGTTCTGGTTCCCGGCGCCGGAGTTCKGCGGGTGCTTCT 785
```
```
Qy    781 ACGGCCTTTGCCCAGAGTTGACAGAGGCAGCAGTTGACGAGGCGCACACCGTTTTCCC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838
```

Qy   841 GCCTTTCTGGAGGAGGGGCCCGAGGAAGAAACAGTGCCTAYGAGGTTGACGAGGCGCAGT---TGYGTCTCGGCTTG 900
Db   839 GCCTTTCTGGAGGAGG--CCGGAGAAACAGTGCCTAYGAGGTTGACGAGGCGCAGT---TGYGTCTCGGCTT 893
```
```
Qy   753 TGCGGAGATCCAGTGGTTCACCTCAGCACCGGCCTTTGCCCAGGAGTTGACGAGGTTGACGAGGCGCAGTTGGG 812
Db   724 TGCCGAGATCMACGTGGTTCACYTCAGMACCGGCCTTTGCCCAGGAGTTGACGAGGCGCAGTTGGG 665
```

```
http://www.macque.org
PCR Primers
FORWARD:  CCCTCACTAAAGGGAACAAAA
FORWARD:  CACTATAGGGCGAATTGGGTA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 971     Std Error: 0.00
Plate: CL000413  row: A  column: 10
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.
```

FEATURES   Location/Qualifiers
     source   1..971
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9544"
                     /clone="IBIUW.17608"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze MMII"
                     /note="Organ: ileum; Vector: pDONR 222; Site_1: BsrG I;
                     Site_2: BsrG I; Created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"

ORIGIN

```
Query Match        52.4%;   Score 797;  DB 7;  Length 971;
Best Local Similarity   93.0%;   Pred. No.'1.2e-189;
Matches 890;  Conservative  0;  Mismatches  60;  Indels  7;  Gaps  5;
```

```
Qy    212  GTGAAGAGAGATTCACCCAGGAGGAGGAGGATCCACCCGGAGGAGGAGGATCTACCTGGAGGAGG   271
           |||||||||||||||||||||||| ||||||||||||||||||||| ||||  |||||||||||
Db      4  GGGAAGAGTGACCCACTGCATGAGGAGGGGGATCTGCCCCAGTGAAGAGGGATCCACCCAGAGAGG    63

Qy    272  AGGGATCTACCTGGAGGAGGAGGATCCACCCGGAGGAGGAGGATCTACCTGAAGTTAAGCCTAAAT   331
Db     64  AGGGATCCACCCAGGAGGAGGATCTACCTGGAGGAGGAGGATCTACCTGAAGTTAAGCCTAAAT   123

Qy    332  CAGAGAGGATCCTTCCTGGAGAATG                                           391
Db    124  CCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTGGGCTCCTGGAGATCCTCAAGAACCCAGA    183

Qy    392  ATAATGCCCACAGGGGACAAAAGAAGGGGGATGACCAGAGTCATTGGGCCTATGGGAGGCGACC    451
Db    184  ATAATGCCCACAGGGACAAAAGAAGGGGGATAACCAGAGACACTGGGCCTATGGGAGGCGACC    243

Qy    452  CGCGGCCTGGCCCCGGGGTGTCCCCAGCCTGCGCGCGGGCGCGCTTCCAGTGCCCCGGGGTGGATATCC    511
Db    244  CGCCCTGGGCCCCAGGTGTCCCCAGCCTGCGGCGGGGGCGCGCTTCCAGTGCCCCGGGGTAGATATCC    303

Qy    512  GCCCCCAGCTCGCCGCGCCTTCTGCCCCGGGCCGCGCCTGCGCCCCCGGAGAACTCTCTGGGCTTCCAGC    571
Db    304  GCCCCCAGCTCGCCGCGCCTTCTGCCCCGGGCTCCGGGGAGTCCGGGGGTACCGGGGCTGCATC    363

Qy    572  TCCCGCGCCGGTTCCCCAGAACTGGCGCCTGCGCCTGCGGAACGAATGGGCCACAGTGTGCAACTGACCTGC    631
Db    364  TCCCGCGCTGCTCCCAGAACTGGCGCCTGCGCCTGCGGAACAAATGGGCCACAGTGTGCAACTGACCTGC    423

Qy    632  CTCCTGGGCTAGAGATGGGCTCTGGGTGCCGGAGTACCGGGGCTCTCCAGCTGCATC    691
Db    424  CTTCCGGGCTTAGAGATGGGCTCTGGGGTCCCGGGGAGTACCGGGGCTCTCTGCATC    483

Qy    692  TGCACTGGGGGGGGTGCAGCTGCGTCCCGGGCCGCACACTGTTGGAAGGCCACCGTTTCC    751
Db    484  TGCACTGGGTGCTGTAGGTGCTGCCGGGCTCGGAGCACACTGTGGAAGGCCACCGTTTCC    543

Qy    752  CTGCCGAGATCCACGTGGTTGTCACCTCAGCACCGGCCTTTGCCAGGAGTTGACGAGGCCTGG    811
Db    544  CTGCCGAGATCCACGTGGTTCACATCAGCACCGCCGCCTTTGCCAGGAGTTGACGAGGCCTGG    603

Qy    812  GGCG-CCCCGGGAGGCGCCTGGCCGCGTTGGGCCCCGCCTTTTCTCGGAGGCGGGGAGAAAAAC    870
Db    604  GGGCCGCCCCCGGAGGCCTGGCCGCGTTTGGCCCGCCTTTTCTCGGAGGAGGGGGGAGAAAAC    663

Qy    871  AGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAGAAAATCGCTGGAGGAGGAAGGCTCAGAGACT    930
```

RESULT 12
CO579387
COS79387
LOCUS   CO579387   971 bp   mRNA   linear   EST 20-JUL-2004
DEFINITION ILLUMIGEN MCQ 50239 Katze MMIL Macaca mulatta cDNA clone
            IBIUW.17608 5' similar to Bases 6 to 971 highly similar to human
            CA9 (Hs.63287), mRNA sequence.
ACCESSION   CO579387
VERSION   COS79387.1 GI:5041031317
KEYWORDS   EST.
SOURCE   Macaca mulatta (rhesus monkey)
  ORGANISM Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;.
            Cercopithecinae; Macaca.
REFERENCE   1 (bases 1 to 971)
  AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
  TITLE   Large-scale Rhesus Macaque cDNA Sequencing
  JOURNAL   Unpublished (2003)
COMMENT   Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.15. 725 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see

```
Qy     64  TGAGAAGCCAGCCAGAGAGCATCTGAGGGGGGAGCCGRGTRAAMTGNCCNGGCC    15
Db     64  TGAGAAGCCAGCCAGAGAGCATCTGAGGGGGGAGCCGGTPAAMTGNCCNGGCC

Qy    124  GAGCTACCGCCGCCCAGCAGCAGGTAGCCGGANACTGGAGCCTGGAATCTTGGGAGNATG    65
Db    124  GAGCTACCGCCGCCGANACTGGAGCCTGGAATCTTGGGAGNATG

Qy   1353  GAGCTACCGCCCCAGCAGCAGGTAGCCGGAAGCTGGAGGCGGAACAGCCAGAGGGCT   1412
Db    184  CAGCGTGCCGTNCCTTGNGCAGTTGACATCCTTTTGGGCTCTTTTTTGCTGTGTCAC    125

Qy   1293  CAGGCGTGCGGTTCCTTGTGTGCAGATGAGAAGGGACGAGGATCTACCTGAAGTTAAGCCTAAATCAGAGAGGATCTCACCCAGTGA   1352
Db    184  CAGGCGTGCGGTNCCTTGNGCAGTTGACATCCTTTTGGGCTCTTTTTTGCTGTGTCAC    125

Qy   1233  TTCCTGCCTGGGCTGGCTGGTGTGACATCCTAGCCCTGGTTTTTGGGCCTTCCTTTTTGCTGTGTCAC   1292
Db    304  GGCCTCCTTCCCGNGCTGGAGTGAACRCGAGTGATGAGCCTGCTGAGCCAGTCCAGCTGAA    245

Qy   1173  GGCCTCCTTCCCTGCTGGAGTGGACAGCAGGTACCTTCGGGAGTGGAGCCAGTCCAGCTGAA   1232
Db    304  GGCCTCCTTCCCGNGCTGGAGTGAACRCGAGTGATGAGCCTGCTGAGCCAGTCCAGCTGAA    245

Qy    364  TAACTCTCGGGCNACAGTCTGGACTTCCGAGGCAGCCCTTGNATGGGCGAGTGATTGA    305

Qy   1113  TGACTCTCGGCTACAGCTTGAACTTCCCAGGCACGACGCACCTTTCTAACACCCTGTGTGGGCCTGG   1172

Qy    424  AACAGTGAATGCTNAGTGCTAAGCAGCTCCACACCTTTCTAACACCCTGTGTGGAGACCTGG    365

Qy   1053  GACAGTGATGCTGGAGTGTCTAAGCAGCTCCACACCCTCTTCTGACACCCGTGTGGGGACCTGG   1112

Qy    484  TGAGGGGTTTCTAACTACACCCCCGTGTGCCCAGGGGTGTCATCTGNACTGTGTTTAACCA    425

Qy    993  TGAGGGGTCTCTGACTACACCCGCCCCTGTCCCCAGGGGTCACCGGGTCATCTGGACTGTGTTTAACCA   1052

Qy    933  GGTCCCAGGACTGGACATATCTGCACTCCTGCCCTCTGACTTCAGCCGCTACTTCCAATA    992

Qy    544  GGTCCCAGAACTGAACATNTCTGNACNCCTGCCCTCTGACTTCAGCCGCTACTTCCAATT    485

Qy    873  TGCCTATGAGCAGTTGCTGTCTCGCTTGGCGCGCCCGTTGGGCCGCGCCCTTTTCTCGGAGGAGGAGGGGCGGGGAGAAAACAG    872

Qy    604  TGCCTATGRGNAGTNGCTNTCTCGGCTTGGAGAAAATCGCTGAGGNAGGCTNAGAACTCA    545

Qy    664  GCGCCCGGAAGCCGTGTTGGGCCGGCCCTTTCTCGGAGGAGGGGCCGGGAAGAAAAACAG    605

Qy    813  GCGCCCGGGGAGGCGCCTGCCGCGTGTTGGGCCGCGCCCCGGAAGAAGAAAAACAG    872
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RESULT 13

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LOCUS       AL577748/c
```

AL577748   994 bp   mRNA   linear   EST   07-APR-2004

```
DEFINITION  AL577748 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK007YK10 3-PRIME, mRNA sequence.
ACCESSION   AL577748
VERSION     AL577748.3  GI:46256749
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 994)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:31316001.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5300.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DK007BF05NP1&c=5300.f.
FEATURES             Location/Qualifiers
     source          1..994
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK007YK10"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match   52.2%;   Score 794.4;   DB 1;   Length 994;
Best Local Similarity   86.3%;
Matches 852;   Conservative 46;   Mismatches 84;   Indels 5;   Gaps 4;

```
Qy    664 AGTGCCTPATGAGCAGTTGCTGTCTCACTTGGAAGAAATCGCTGAGGAAGGCTTCAGAGACT 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 CAGGTCCCAGGACTGGGACAGATATCTGCACTCCTGCCCTGCTCAGCGCTACTTCCAA 990

Qy    724 CACGTCCCAGGACTGGGACGTATCTGCACTCAGCCGTTCTT GAGCCGCTACTTCCGA 783
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 TATGAGGGGGTCTCTGACTACACGGCGCCCTGTGCCCAGGGGTGTCATCT-GGACTGTGTTPAA 1049

Qy    784 TATGAGGGGGTCTTCTGACTACACGGCGCCCTGTGCCCAGGGGTGTCATCT-GGACTGTGTTTA 843
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 CCAGACAGTGATGCTGAGTGCTGAGTGCTTAAGCAGCAGCTCCACAGCTCCACCCCCAGGGGAC 1108

Qy    844 CCAGACAGTGATGCTGAGTGCTGAGTGCTTAAGCAGCAGCTCCACAGCTCCACCCCCAGGGGAC 903
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1050 CCAGACAGTGATGCTGAGTGCTGAGTGCTTAAGCAGCAGCTCCACAGCTCCACCCCCAGGGGAC 1108

Qy    904 CTGGGGGACTCTCCGGCTACGGCTGAACTTCCTGAAGGGGACCCACCCCTTGGAATGGG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 CTGGGTGACTCT--CGGCTACAGCTGAACTTCC---GAGCGACGGACGGCGGGGGGGGG 1161
```

RESULT 14

```
LOCUS       AL580216/c
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AL580216   1017 bp   mRNA   linear   EST   07-APR-2004

```
DEFINITION  AL580216 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
            Homo sapiens cDNA clone CS0D005YK14 3-PRIME, mRNA sequence.
ACCESSION   AL580216
VERSION     AL580216.2  GI:31318495
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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Qy    925 CYYCCGMGVACTCTCCTCKCMACNAAKGGCCCACA-KGTGCMAYTGMCCYTISCYGCYKGGGC 867
          ::|:::|||||  ||| |: ::||||||:::::||| :::|||: |:|: :::||:  |:|:|||
Db    627 GGACTGGACATATCTGCACTCCTGCCCTGCTCAGCGCTACTTCCAAATATGAGGGG 568

Qy    866 KAGAGATGGCTCTTGGGTCCGGGGGGGGGGTACGGGGTCTTGCGAGCTGCGCATCT-GCACTGG 807
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627 GGACTGGACATATCTGCACTCCTGCCCTGCTCAGCGCTACTTCCAAATATGAGGGG 568
```

ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1017)
  AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL Unpublished (2001)
COMMENT   On Feb 16, 2001 this sequence version replaced gi:12946023.
           Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
           1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
           end enriched, double-strand cDNA was digested with Not I and cloned
           into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
           was normalized. Library was constructed by Life Technologies, a
           division of Invitrogen. This sequence belongs to sequence cluster
           5300.f.
           For more information about this cluster, see
           http://www.genoscope.cns.fr/cdna?s=CS0DJ005BP07NP1&c=5300.f.
FEATURES   Location/Qualifiers
     source   1..1017
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ005YK14"
                     /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
                     /cell_line="JURKAT"
                     /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
                     10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match   51.9%;   Score 789.4;   DB 1;   Length 1017;
Best Local Similarity   87.9%;
Matches 832;   Conservative   44;   Mismatches   66;   Indels   4;   Gaps   3;

Qy   545 GCCCCCTGGAACTCCTCGGCTTCCAGCTCCCCGGCCTTCCCACGGAACTGGGCCTCGCAACA 604
             ||||||||||||||||||||||||| |||| || ||||| | ||||||||||||| |||||
Db   943 GCGCCCCTGAACTCCTGGS--TTCCASTCCGCGCGCTCCCAGAACTGGCCCTGCGCAAACA 886

Qy   605 ATGGCCACAGTGTGCAACTGACCCTGCCT--CCTGGGCTAGAGATGAGCCTCTGGGGTCCCGGG 663
             ||||||||||||||||||||||||||| || |||||||||| ||||| |||||||||||||
Db   885 ATGGCCACAGTGTGCAACTGACCCTGCCTCCCGGGGGTTCCCCGGG 826

Qy   664 CGGGAGTACCGGGGCCTCTGCAGCTGCATCTTGCACTGGGGGGGGGGCGCAGTTGCGTTCCGGGGCTCG 723
             ||||||| |||||||||||||||||||| |||||||||||| |||||||||||||||||||
Db   825 CGGGAGKTACYGGGGCCTCTGCAGCTTGCACTYGGACCTTGCGTCGTTCGGGGCTCG 766

Qy   724 GAGCACACTGTGGAAGGCCACCCTTTCCCTGCCGGAGATCCACGTGGTTCACCTCAGCACC 783
             |||||||||||||||||||||||||||||| ||||| ||| |: || |||||: |:|:
Db   765 GAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGGAGATCCACVARAAMMAMMMMAANAMA 706

Qy   784 GCCTTTGCCGAGTTGACGAGGCCTTGGGGGCCCGGGGGAGGCCTTGGCCGGTGTTGGCCGCC 843
             ||||| ||||||||||||| || |||||||| || ||||||||||||||||||||||||||
Db   705 VCCHAACCARAGTTGACGAGGCCTTGGGCCCGGTNTTNNCCNCC 646

Qy   844 TTTCTGGAGGAGGGGGCCCGGAGAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAA 903
             |||||||||||||||||| || ||||||||| || |||||||||: |||| :||: |:|:
Db   645 TTTCTNGAGNAGGNCCCGNAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGGAA 586

Qy   904 GAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGTATCTGCACTCCTG 963
             ||||| || ||||||||||||||| |||||||| :||: |||||||||||||||||
Db   585 GAAATCCCTGAGGAAGGCTCTAGAGACTCAGTGRACACMCCCCACTCCTG 526

Qy   964 CCCTCTGACTTCAGCCGTTACTTCCAATATGAGGGGGTCTTGACTACACCGCCCGTCGTTCC 1023
             ||||| |||||||||||||||||||| ||: ||: |||||||||||||||||||||||||
Db   525 CCCTCTGACTTCAGCCGTTACTTCCAATAATGAGGGGGTCTCTGACTACACCGCCCGTGCC 466

Qy   1024 CAGGGTGTCATCTGGACTNGTGTTTAACCAGACAGTGATGCTGTGAGTGTGCTAAGCAGCTCCAC 1083

Db   465 CAGGGTGTCATCTGGACTGCTGTGTTTAACCAGACAGTGATGGCTGGACTGGCTAAGCAGCTCCAC 406
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1084 ACCCTCTCTGACACCCTGTGGGGGACCTGGTGGTGACTTCGCGTACAGCTGAACTTCGAGCG 1143
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   405 ACCCTCTCTGACACCCTGTGGGGGACCTGGTGGTGACTCTCGGCCGGCTACAGCTGAACTTCCGAGCG 346

Qy   1144 ACGCAGCCTTTGAATGGGCGGAGTGAGATTGAGGGCCTTCCTTCCCTGCTTCGTTGGGACCAGCAGT 1203
             ||| | |||||||||||||||||||:||||||||||:|||||||||||:||:||||||:|||||||
Db   345 ACGCAGCCTTTGAATGGGCGGAGTGATTGAGGGCCCCCCTTCCCTTCCCTGCTTCGTTGGGACGCAGA 286

Qy   1264 CTGGTTTTTTGGCCCTTCCTTTTTGCGTGTCACCAGGCGTGCGCGCGTTCGTGCTGGTGCAGATAGAAGG 1323
             ||:| |||||||:|||||||||||||||||||||||||||:|||||||||||:||||||||||||||||
Db   285 CCTCGGGGCYGCTGAGCCAGCCAGTCACAGADAATTCNYDCCTGSGCTGCGTCGTGGTVACAHCCTAGCC 226

Qy   1324 CAGCACAGAAGGGGGAACCRAAAGGGGGTGAGCTTACCCGCCCCAGCAGGAGGGAGCCGGAGGAGGACT 1383
             ||:| |||||||||||||||||||||||||||::|||||||||||||||||||||||||||:|:|||
Db   225 CTRAHYTTNGGGCCYCCCYCCTTTTTGGCTGCTGTCACCATCKYCGCGGGTTTCCTTGTGCAGATGAAGG 166

Qy   1444 GCCGGTAACTGTGTCCTGCTCTGTCCTTGTTTAATGCCGCCACTTCCTTTTTAACT 1489
             | ||||||||| || ||||||||:|||||||||:| |||||||||||||||||||
Db   46 GCGGGGTGNGNGKCGTGGCCTGSWNATNATGCVAGTTCCTTWTAACT 1

RESULT 15
LOCUS   AL555184   927 bp   mRNA   linear   EST 30-MAR-2004
DEFINITION AL555184 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK007YK10 5-PRIME, mRNA sequence.
ACCESSION   AL555184
VERSION   AL555184.3   GI:45859924
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 927)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   On Feb 15, 2001 this sequence version replaced gi:31276993.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr; Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5300.f.
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DK007BF05QP1&c=5300.f.
FEATURES   Location/Qualifiers
     source   1..927
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK007YK10"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V

ORIGIN

sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match   50.8%; Score 772.6; DB 1; Length 927;
Best Local Similarity   96.0%; Pred. No. 1.7e-183;
Matches 840; Conservative 5; Mismatches 24; Indels 6; Gaps 5;

```
Qy      1 ACAGTCAGCCCGGCAATGGCTTCCCTGTGCCCCAGTCCCTTGTTTGAATCCCCGGCC   60
            ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db     20 ACAGTCAGCCGCCAATGG-TCCCCTGTGCCCCAGCCCTTGGCTCCCCTCTTGGTTGAATCCCCGGCC   78

Qy     61 CCTGCTTCCAGGCCTCACTGTGCAACTGCTCGTGCTCAACTGCTTTCTTGATGCCTGTCCAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 CCTGCTTCCAGGCCTCACTGTGCAACTCGTGCTCGTGCTCAACTGCTTTCTTGGTGCCTGTCCAT  138

Qy    121 CCCCAGAGGGTTGCCCCGGATGCAGGAGGAGGGAGGCTCTTCTGGGGAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 CCCCAGAGGGTTGCCCCCGGATGCAGGAGGAGGGAGGCTCTTCTGGGGAA  198

Qy    181 GATGACCCACTGGGCGCAGGAGATCTGCCTCACTGTGCTTCTTCGATGCCTTCTTGGTGCCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 GATGACCCACTGGGCGCAGGAGATCTGCCTCAGTGAACAGGAGGATTCACCCAGACGAGGAGGAT  258

Qy    241 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGAGGATCTACCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 CCACCCCGGAGGAGGAGGATCTACCTGGAGGAGGAGGAGGAGGATCTACCT  318

Qy    301 GAAGTTRAGCCTARAATCAGAAGAGAGAGAGGGGCTCCCTGAAGTTRAGGATCTACCTACTGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 GAAGTTRAAGCCTRAAATCAGAAGAGAGAGGGGCTCCCTGAAGTTRAGAGGATCTACCTACTGTT  378

Qy    361 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCCAGAGGACAAAGAAAGGGGAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GAGGCTCCTGGAGATCCTCAAGAACCCCAGAATAAATGCCCACAGGGACAAAGAAAGGGGAT  438

Qy    421 GACCAGAGTCATTGGCCTATGGAGGGGACCCGCCCCGGGGGTGTCCCCAGCCTGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 GACCAGAGTCATTGGCCTATGGAGGGGACCCGCCCCGGGGGTGTCCCCAGCCTGC  498

Qy    481 GCGGGCCCGCCTTCCAGTCCCGGTGGATATCCGGCCCCCAGCTCCGCCCTTCTGCCCGCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 GCGGGCCCGCCTTCCAGTCCCGGGGAATATCCGGCCCCCAGCTCCGCCCTTCTGCCCGCC  558

Qy    541 CTGCGCCCCCTGGAACTCCTGGGGCTTCCAGCTCTCCAGCTCCCAGAACTGCGCCTCGCG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 CTGCGCCCCCTGGAACTCCTGGGGCTTCCAGCTCTCCAGCTCCCAGAACTGCGCCTCGCG  618

Qy    601 AACAATGGCCACAGTGTGCAACTGACCCTGCCTTCCCTGGCTAGAGATGGCTCTGGGGTCCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 AACAATGGCCACAGTGTGCAACTGACCCGTTTCCCTGCCTAGAGATGGCTCTGGGGTCCC  678

Qy    661 GGGGCGGGGAGTACCGGGGCTCTGCAGCTGCATCTGCACT-GGGGGGCTGGCAGGTTCGTCCCGGG  719
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 GGGGCGGGGAGTACCGGGGCTTCGCAGCTGCATCTGCACTGGGGGGCTGCAGGGTCGTCCCGGG  738

Qy    720 CTCGGACCACACTGTGGAAGGCCACACGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAG  779
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 CTCGGAGGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCA-CYCAG  797

Qy    780 CACCGGCCTTTGCCAGAGTTGACGAGGCGGCCTTGGGGCGGCAGGAGGCCTTGGCCGTGTTGGC  839
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 CACASCTTTTGCCAGAGTTGACGAGG-CTTKGGGCGCGCCGGGGAGGC--TGGCGTGTTGGC  854

Qy    840 CGCCTTTCTGGAGGAGGGGCCCGGAAGAGAAACAGTG  874
            ||  |||   |||    ||  |||||||||||||||
Db    855 GCYTTYTGGAGGAGGGGCCCGGAGAAAAGTGCTATG  889
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